



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>7</sup> :</b> <b>C12N 15/12, C07K 14/47, C12Q 1/68, A61K 39/395, G01N 33/68, 33/574, C07K 16/30, C12N 15/62, 5/02 // A61P 35/00</b>		<b>A2</b>	<b>(11) International Publication Number:</b> <b>WO 00/04149</b> <b>(43) International Publication Date:</b> 27 January 2000 (27.01.00)																					
<b>(21) International Application Number:</b> PCT/US99/15838 <b>(22) International Filing Date:</b> 14 July 1999 (14.07.99)  <b>(30) Priority Data:</b> <table border="0"><tr><td>09/115,453</td><td>14 July 1998 (14.07.98)</td><td>US</td></tr><tr><td>09/116,134</td><td>14 July 1998 (14.07.98)</td><td>US</td></tr><tr><td>09/159,822</td><td>23 September 1998 (23.09.98)</td><td>US</td></tr><tr><td>09/159,812</td><td>23 September 1998 (23.09.98)</td><td>US</td></tr><tr><td>09/232,880</td><td>15 January 1999 (15.01.99)</td><td>US</td></tr><tr><td>09/232,149</td><td>15 January 1999 (15.01.99)</td><td>US</td></tr><tr><td>09/288,946</td><td>9 April 1999 (09.04.99)</td><td>US</td></tr></table> <b>(71) Applicant:</b> CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).  <b>(72) Inventors:</b> DILLON, Davin, Clifford; 21607 N.E. 24th Street, Redmond, WA 98053 (US). HARLOCKER, Susan, Louise; 6203 20th Avenue N.W., Seattle, WA 98107 (US). YUQIU, Jiang; 5001 South 232nd Street, Kent, WA 98032 (US). XU, Jiangchun; 15805 S.E. 43rd Place, Bellevue, WA 98006 (US). MITCHAM, Jennifer, Lynn; 16677 Northeast 88th Street, Redmond, WA 98052 (US).			09/115,453	14 July 1998 (14.07.98)	US	09/116,134	14 July 1998 (14.07.98)	US	09/159,822	23 September 1998 (23.09.98)	US	09/159,812	23 September 1998 (23.09.98)	US	09/232,880	15 January 1999 (15.01.99)	US	09/232,149	15 January 1999 (15.01.99)	US	09/288,946	9 April 1999 (09.04.99)	US	<b>(74) Agents:</b> MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).  <b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
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09/288,946	9 April 1999 (09.04.99)	US																						
<b>(54) Title:</b> COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER  <b>(57) Abstract</b>  Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.																								

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## COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER

### TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

### SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present

invention provides polypeptides comprising at least a portion of a prostate tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and a non-specific immune response enhancer.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a non-specific immune response enhancer.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.



Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited

above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic

kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate tumor polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate tumor polypeptide P502S. In each case, the number of  $\gamma$ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate tumor polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8<sup>+</sup> cell line (3A-1) for a representative prostate tumor antigen (P501S). Figure 6A shows the results of a <sup>51</sup>Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12  
SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16  
SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1  
SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9  
SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4  
SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17  
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17  
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12  
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12  
SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862  
SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862  
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13  
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13  
SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19  
SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19  
SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25  
SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25  
SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24  
SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24  
SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58  
SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58  
SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63  
SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63  
SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4  
SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4  
SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14  
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14  
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12  
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16  
SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21  
SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48  
SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55  
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2  
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6  
SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858  
SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860  
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864  
SEQ ID NO: 41 is the determined cDNA sequence for P5  
SEQ ID NO: 42 is the determined cDNA sequence for P8  
SEQ ID NO: 43 is the determined cDNA sequence for P9  
SEQ ID NO: 44 is the determined cDNA sequence for P18  
SEQ ID NO: 45 is the determined cDNA sequence for P20  
SEQ ID NO: 46 is the determined cDNA sequence for P29  
SEQ ID NO: 47 is the determined cDNA sequence for P30  
SEQ ID NO: 48 is the determined cDNA sequence for P34  
SEQ ID NO: 49 is the determined cDNA sequence for P36  
SEQ ID NO: 50 is the determined cDNA sequence for P38  
SEQ ID NO: 51 is the determined cDNA sequence for P39  
SEQ ID NO: 52 is the determined cDNA sequence for P42  
SEQ ID NO: 53 is the determined cDNA sequence for P47  
SEQ ID NO: 54 is the determined cDNA sequence for P49  
SEQ ID NO: 55 is the determined cDNA sequence for P50  
SEQ ID NO: 56 is the determined cDNA sequence for P53  
SEQ ID NO: 57 is the determined cDNA sequence for P55  
SEQ ID NO: 58 is the determined cDNA sequence for P60  
SEQ ID NO: 59 is the determined cDNA sequence for P64  
SEQ ID NO: 60 is the determined cDNA sequence for P65  
SEQ ID NO: 61 is the determined cDNA sequence for P73  
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SEQ ID NO: 64 is the determined cDNA sequence for P79  
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SEQ ID NO: 67 is the determined cDNA sequence for P80  
SEQ ID NO: 68 is the determined cDNA sequence for P82  
SEQ ID NO: 69 is the determined cDNA sequence for U1-3064  
SEQ ID NO: 70 is the determined cDNA sequence for U1-3065  
SEQ ID NO: 71 is the determined cDNA sequence for V1-3692  
SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905  
SEQ ID NO: 73 is the determined cDNA sequence for V1-3686  
SEQ ID NO: 74 is the determined cDNA sequence for R1-2330  
SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976  
SEQ ID NO: 76 is the determined cDNA sequence for V1-3679

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SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785  
SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787  
SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796  
SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807  
SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810  
SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811  
SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876  
SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884  
SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896  
SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761  
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SEQ ID NO: 98 is the determined cDNA sequence for 1H-4772  
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SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280  
SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12 (also referred to as P504S)  
SEQ ID NO: 108 is the predicted amino acid sequence for F1-12  
SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17  
SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12  
SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862  
SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

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SEQ ID NO: 169 is the determined cDNA sequence for P235  
SEQ ID NO: 170 is the determined cDNA sequence for P243  
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SEQ ID NO: 172 is the predicted amino acid sequence for P703P-DE1  
SEQ ID NO: 173 is the determined cDNA sequence for P703P-DE2  
SEQ ID NO: 174 is the determined cDNA sequence for P703P-DE6  
SEQ ID NO: 175 is the determined cDNA sequence for P703P-DE13  
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SEQ ID NO: 177 is the determined cDNA sequence for P703P-DE14  
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SEQ ID NO: 182 is the determined extended cDNA sequence for 1G-4744  
SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-4774  
SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-4781  
SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-4785  
SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-4787



SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-4796  
SEQ ID NO: 188 is the determined extended cDNA sequence for 1I-4807  
SEQ ID NO: 189 is the determined 3' cDNA sequence for 1I-4810  
SEQ ID NO: 190 is the determined 3' cDNA sequence for 1I-4811  
SEQ ID NO: 191 is the determined extended cDNA sequence for 1J-4876  
SEQ ID NO: 192 is the determined extended cDNA sequence for 1K-4884  
SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-4896  
SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-4761  
SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-4762  
SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-4766  
SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770  
SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771  
SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-4772  
SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309  
SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278  
SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288  
SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283  
SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304  
SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296  
SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280  
SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd  
SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con  
SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev  
SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd  
SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev  
SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd  
SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev  
SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd  
SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev  
SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd  
SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev  
SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd  
SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev  
SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev  
SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd  
SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev  
SEQ ID NO: 223 is the determined cDNA sequence for P509S

SEQ ID NO: 224 is the determined cDNA sequence for P510S  
SEQ ID NO: 225 is the determined cDNA sequence for P703DE5  
SEQ ID NO: 226 is the determined cDNA sequence for 9-A11  
SEQ ID NO: 227 is the determined cDNA sequence for 8-C6  
SEQ ID NO: 228 is the determined cDNA sequence for 8-H7  
SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13  
SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14  
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23  
SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24  
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25  
SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30  
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34  
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35  
SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36  
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38  
SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39  
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40  
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41  
SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42  
SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45  
SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46  
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51  
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56  
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64  
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65  
SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67  
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76  
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84  
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85  
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86  
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87  
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88  
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1  
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2  
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2  
SEQ ID NO: 259 is the determined cDNA sequence for JP1B1  
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2

SEQ ID NO: 261 is the determined cDNA sequence for JP1D3  
SEQ ID NO: 262 is the determined cDNA sequence for JP1A4  
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5  
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6  
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6  
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5  
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6  
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8  
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7  
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9  
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10  
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9  
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12  
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12  
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11  
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11  
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12  
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12  
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12  
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2  
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1  
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2  
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3  
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4  
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3  
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4  
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6  
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6  
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5  
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8  
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7  
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7  
SEQ ID NO: 293 is the determined cDNA sequence for P8D8  
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7  
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8  
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8  
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10

SEQ ID NO: 298 is the determined cDNA sequence for JP8C10  
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9  
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10  
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9  
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9  
SEQ ID NO: 303 is the determined cDNA sequence for JP8C12  
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11  
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12  
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12  
SEQ ID NO: 307 is the determined cDNA sequence for P711P  
SEQ ID NO: 308 is the determined cDNA sequence for P712P  
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23  
SEQ ID NO: 310 is the determined cDNA sequence for P774P  
SEQ ID NO: 311 is the determined cDNA sequence for P775P  
SEQ ID NO: 312 is the determined cDNA sequence for P715P  
SEQ ID NO: 313 is the determined cDNA sequence for P710P  
SEQ ID NO: 314 is the determined cDNA sequence for P767P  
SEQ ID NO: 315 is the determined cDNA sequence for P768P  
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes  
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5  
SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5  
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26  
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26  
SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23  
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23  
SEQ ID NO: 332 is the determined full length cDNA sequence for P509S  
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)  
SEQ ID NO: 334 is the determined cDNA sequence for P714P  
SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)  
SEQ ID NO: 336 is the predicted amino acid sequence for P705P  
SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10  
SEQ ID NO: 338 is the amino acid sequence of the peptide p5  
SEQ ID NO: 339 is the predicted amino acid sequence of P509S  
SEQ ID NO: 340 is the determined cDNA sequence for P778P  
SEQ ID NO: 341 is the determined cDNA sequence for P786P  
SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

SEQ ID NO: 381 is the determined cDNA sequence for B716P.

SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.

SEQ ID NO: 383 is the predicted amino acid sequence for P711P.

SEQ ID NO: 384 is the cDNA sequence for P1000C.

SEQ ID NO: 385 is the cDNA sequence for CGI-82.

SEQ ID NO:386 is the cDNA sequence for 23320.

SEQ ID NO:387 is the cDNA sequence for CGI-69.

SEQ ID NO:388 is the cDNA sequence for L-idoitol-2-dehydrogenase.

SEQ ID NO:389 is the cDNA sequence for 23379.

SEQ ID NO:390 is the cDNA sequence for 23381.

SEQ ID NO:391 is the cDNA sequence for KIAA0122.

SEQ ID NO:392 is the cDNA sequence for 23399.

SEQ ID NO:393 is the cDNA sequence for a previously identified gene.

SEQ ID NO:394 is the cDNA sequence for HCLBP.

SEQ ID NO:395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553.

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.  
SEQ ID NO:415 is the cDNA sequence for 22572.  
SEQ ID NO:416 is the cDNA sequence for 22573.  
SEQ ID NO:417 is the cDNA sequence for 22573.  
SEQ ID NO:418 is the cDNA sequence for 22575.  
SEQ ID NO:419 is the cDNA sequence for 22580.  
SEQ ID NO:420 is the cDNA sequence for 22581.  
SEQ ID NO:421 is the cDNA sequence for 22582.  
SEQ ID NO:422 is the cDNA sequence for 22583.  
SEQ ID NO:423 is the cDNA sequence for 22584.  
SEQ ID NO:424 is the cDNA sequence for 22585.  
SEQ ID NO:425 is the cDNA sequence for 22586.  
SEQ ID NO:426 is the cDNA sequence for 22587.  
SEQ ID NO:427 is the cDNA sequence for 22588.  
SEQ ID NO:428 is the cDNA sequence for 22589.  
SEQ ID NO:429 is the cDNA sequence for 22590.  
SEQ ID NO:430 is the cDNA sequence for 22591.  
SEQ ID NO:431 is the cDNA sequence for 22592.  
SEQ ID NO:432 is the cDNA sequence for 22593.  
SEQ ID NO:433 is the cDNA sequence for 22594.  
SEQ ID NO:434 is the cDNA sequence for 22595.  
SEQ ID NO:435 is the cDNA sequence for 22596.  
SEQ ID NO:436 is the cDNA sequence for 22847.  
SEQ ID NO:437 is the cDNA sequence for 22848.  
SEQ ID NO:438 is the cDNA sequence for 22849.  
SEQ ID NO:439 is the cDNA sequence for 22851.  
SEQ ID NO:440 is the cDNA sequence for 22852.  
SEQ ID NO:441 is the cDNA sequence for 22853.  
SEQ ID NO:442 is the cDNA sequence for 22854.  
SEQ ID NO:443 is the cDNA sequence for 22855.  
SEQ ID NO:444 is the cDNA sequence for 22856.  
SEQ ID NO:445 is the cDNA sequence for 22857.  
SEQ ID NO:446 is the cDNA sequence for 23601.  
SEQ ID NO:447 is the cDNA sequence for 23602.  
SEQ ID NO:448 is the cDNA sequence for 23605.  
SEQ ID NO:449 is the cDNA sequence for 23606.  
SEQ ID NO:450 is the cDNA sequence for 23612.

SEQ ID NO:451 is the cDNA sequence for 23614.  
SEQ ID NO:452 is the cDNA sequence for 23618.  
SEQ ID NO:453 is the cDNA sequence for 23622.  
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.  
SEQ ID NO:455 is the cDNA sequence for LIM protein.  
SEQ ID NO:456 is the cDNA sequence for a known gene.  
SEQ ID NO:457 is the cDNA sequence for a known gene.  
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.  
SEQ ID NO:459 is the cDNA sequence for 23045.  
SEQ ID NO:460 is the cDNA sequence for 23032.  
SEQ ID NO:461 is the cDNA sequence for 23054.  
SEQ ID NOs:462-467 are cDNA sequences for known genes.  
SEQ ID NOs:468-471 are cDNA sequences for P710P.  
SEQ ID NO:472 is a cDNA sequence for P1001C.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate tumor protein or a variant thereof. A "prostate tumor protein" is a protein that is expressed in prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain prostate tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.



The present invention is based on the discovery of human prostate tumor proteins. Sequences of polynucleotides encoding certain tumor proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Sequences of polypeptides comprising at least a portion of a tumor protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

#### PROSTATE TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50,

in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) *Unified Approach to Alignment and Phylogenies* pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to

the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, a prostate tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with  $^{32}\text{P}$ ) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using

standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate tumor protein are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Isolation of these

polynucleotides is described below. Each of these prostate tumor proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such

as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (*e.g.*, avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

#### PROSTATE TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate tumor protein or a variant thereof, as described herein. As noted above, a "prostate tumor protein" is a protein that is expressed by prostate tumor cells. Proteins that are prostate tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from

the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein.

Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are



*E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into

the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as

amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

#### BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, urine and/or tumor biopsies) from

patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g., mice, rats, rabbits, sheep or goats*). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e., reactivity with the polypeptide of interest*). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient

time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and

thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

#### T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (*see also* U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate tumor polypeptide, polynucleotide encoding a prostate tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience

(Greene 1998)). T cells that have been activated in response to a prostate tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Prostate tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to a prostate tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

#### PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998,



and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or

preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- $\beta$ ) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is

quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-

surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a prostate tumor protein (or portion or other variant thereof) such that the prostate tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the prostate tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that

provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

#### CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein

may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100  $\mu$ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such

a response can be monitored by establishing an improved clinical outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

#### METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding

agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.



More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred

embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate tumor polypeptides to

detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with a prostate tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate tumor polypeptide (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate tumor polypeptide to serve as a control. For CD4<sup>+</sup> T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers

comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375 and 381. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

#### DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

## EXAMPLES

### EXAMPLE 1

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70  $\mu$ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100  $\mu$ l of

H<sub>2</sub>O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human

autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted



amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO: 73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and

prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339.

## EXAMPLE 2

### DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that

F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression

in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatazis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

### EXAMPLE 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated

and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A4, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable.

Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX\_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues.



Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

#### EXAMPLE 4 SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

#### EXAMPLE 5

##### FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350-365.

#### EXAMPLE 6

##### PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2.1 (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100µg of P2S#12 and 120µg of an I-A<sup>b</sup> binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL),  $2 \times 10^{-5}$  M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells ( $5 \times 10^5$ /ml) were restimulated with  $2.5 \times 10^6$ /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were

restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2.1 expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2.1 molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200  $\mu\text{g/ml}$  were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2.1 were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 $\mu\text{g}$  of P1S #10 and 120 $\mu\text{g}$  of an I-A<sup>b</sup> binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed ( $2 \mu\text{g/ml}$  P1S#10 and 10mg/ml  $\beta 2$ -microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 $\mu\text{g/ml}$  dextran sulfate and 25 $\mu\text{g/ml}$  LPS for 3 days). Six days later cells ( $5 \times 10^5/\text{ml}$ ) were restimulated with  $2.5 \times 10^6/\text{ml}$  peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and  $3 \times 10^6/\text{ml}$  A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly

basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

#### EXAMPLE 7

##### ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE TUMOR POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8<sup>+</sup> T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8<sup>+</sup> T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a  $\gamma$ -interferon ELISPOT assay (see Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on  $10^4$  fibroblasts in the presence of 3  $\mu$ g/ml human  $\beta_2$ -microglobulin and 1  $\mu$ g/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml  $\gamma$ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a  $\gamma$ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of  $\gamma$ -interferon spots with increasing numbers of T

cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

#### EXAMPLE 8

##### PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate tumor antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 µg VR10132-P501S either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed A2-restricted CTL epitope.

#### EXAMPLE 9

##### GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH PROSTATE TUMOR ANTIGEN

Using *in vitro* whole-gene priming with P501S-retrovirally transduced autologous fibroblasts (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon-γ ELISPOT analysis as described above. Using a panel of HLA-mismatched fibroblast lines transduced with P501S, these CTL lines were shown to be restricted HLA-A2 class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 µg/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and

priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S. Following four stimulation cycles, CD8+ T cell lines were identified that specifically produced interferon- $\gamma$  when stimulated with P501S-transduced autologous fibroblasts. The P501S-specific activity could be sustained by the continued stimulation of the cultures with P501S-transduced fibroblasts in the presence of IL-15. A panel of HLA-mismatched fibroblast lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- $\gamma$  in an ELISPOT assay, the P501S specific response was shown to be restricted by HLA-A2. These results demonstrate that a CD8+ CTL response to P501S can be elicited.

#### EXAMPLE 10

##### IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN A PROSTATE TUMOR ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2 transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of P703P transduced target cells expressing either HLA-A2Kb or HLA-A2. Specifically, HLA-A2 transgenic mice were immunized subcutaneously in the footpad with 100  $\mu$ g of p5 peptide together with 140  $\mu$ g of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with p5 peptide and cultured with GM-CSF and IL-4 together with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis



with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated.

#### EXAMPLE 11

##### EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate tumor and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach).

#### EXAMPLE 12

##### ELICITATION OF PROSTATE TUMOR ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate tumor antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GM-CSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8<sup>+</sup> cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles, CD8<sup>+</sup> lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to

express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays ( $^{51}\text{Cr}$  release) and interferon-gamma production (Interferon-gamma Elispot; *see above* and Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

### EXAMPLE 13

#### IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

Table I  
Summary of Prostate Tumor Antigens

Known Genes	Previously identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-idoitol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang(23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	

transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate

tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

#### EXAMPLE 14

##### IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate tumor antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups, Plus (normal prostate and prostate tumor libraries, and breast cell lines, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

**Table II**  
**Prostate cDNA Libraries and ESTs**

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones found in the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones found in the Plus, Minus and Other group libraries, but the expression in the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones found in Plus, Minus and Other group libraries, but the expression in the Plus group is higher than the expression in the Minus group. This analysis identified 4,345 breast clusters (see Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III  
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor cDNA was at least three times the level in normal prostate cDNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NOs:401-453, with certain novel sequences shown in SEQ ID NOs:407, 413, 416-419, 422, 426, 427 and 450.

Table IV  
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P

403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57



439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

#### EXAMPLE 15

##### FURTHER IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NOs:454-467. Of these sequences SEQ ID NOs:459-461 correspond to novel genes. The others (SEQ ID NOs:454-458 and 461-467) correspond to known sequences.

#### EXAMPLE 16

##### FURTHER CHARACTERIZATION OF PROSTATE TUMOR ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic ABI Sequencer. Four sequences were obtained, and are presented in SEQ ID NOs:468-471.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

## CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339 and 383.

4. An isolated polynucleotide encoding at least 15 amino acid residues of a prostate tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434,

435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

7. An isolated polynucleotide comprising a sequence that hybridizes, under moderately stringent conditions, to a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-7.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An expression vector comprising a polynucleotide according claim 8.

12. A host cell transformed or transfected with an expression vector according to claim 11.

13. A pharmaceutical composition comprising a polypeptide according to claim 1, in combination with a physiologically acceptable carrier.

14. A vaccine comprising a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

15. A vaccine according to claim 14, wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine according to claim 14, wherein the non-specific immune response enhancer induces a predominantly Type I response.

17. A pharmaceutical composition comprising a polynucleotide according to claim 4, in combination with a physiologically acceptable carrier.

18. A vaccine comprising a polynucleotide according to claim 4, in combination with a non-specific immune response enhancer.

19. A vaccine according to claim 18, wherein the non-specific immune response enhancer is an adjuvant.

20. A vaccine according to claim 18, wherein the non-specific immune response enhancer induces a predominantly Type I response.

21. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472 or a complement of any of the foregoing polynucleotide sequences.

22. A pharmaceutical composition comprising an antibody or fragment thereof according to claim 18, in combination with a physiologically acceptable carrier.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

26. A vaccine according to claim 25, wherein the non-specific immune response enhancer is an adjuvant.

27. A vaccine according to claim 25, wherein the non-specific immune response enhancer induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

30. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polynucleotide according to claim 4, and thereby inhibiting the development of a cancer in the patient.

31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antibody or antigen-binding fragment thereof according to claim 21, and thereby inhibiting the development of a cancer in the patient.

32. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.
33. A method according to claim 32, wherein the antigen-presenting cell is a dendritic cell.
34. A method according to any one of claims 29-32, wherein the cancer is prostate cancer.
35. A fusion protein comprising at least one polypeptide according to claim 1.
36. A fusion protein according to claim 35, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.
37. A fusion protein according to claim 35, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.
38. A fusion protein according to claim 35, wherein the fusion protein comprises an affinity tag.
39. An isolated polynucleotide encoding a fusion protein according to claim 35.
40. A pharmaceutical composition comprising a fusion protein according to claim 32, in combination with a physiologically acceptable carrier.
41. A vaccine comprising a fusion protein according to claim 35, in combination with a non-specific immune response enhancer.
42. A vaccine according to claim 41, wherein the non-specific immune response enhancer is an adjuvant.

43. A vaccine according to claim 41, wherein the non-specific immune response enhancer induces a predominantly Type I response.

44. A pharmaceutical composition comprising a polynucleotide according to claim 40, in combination with a physiologically acceptable carrier.

45. A vaccine comprising a polynucleotide according to claim 40, in combination with a non-specific immune response enhancer.

46. A vaccine according to claim 45, wherein the non-specific immune response enhancer is an adjuvant.

47. A vaccine according to claim 45, wherein the non-specific immune response enhancer induces a predominantly Type I response.

48. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 40 or claim 44.

49. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 41 or claim 45.

50. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate tumor protein from the sample.

51. A method according to claim 50, wherein the biological sample is blood or a fraction thereof.



52. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

53. A method for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of:

- (i) a polypeptide according to claim 1;
  - (ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
  - (iii) a polynucleotide encoding a polypeptide of (i) or (ii); and/or
  - (iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii);
- under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

54. An isolated T cell population, comprising T cells prepared according to the method of claim 53.

55. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 54.

56. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

- (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:
  - (i) a polypeptide according to claim 1;
  - (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
  - (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
  - (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

- (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

57. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

- (b) cloning at least one proliferated cell; and
- (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

58. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

59. A method according to claim 58, wherein the binding agent is an antibody.

60. A method according to claim 59, wherein the antibody is a monoclonal antibody.

61. A method according to claim 58, wherein the cancer is prostate cancer.
62. A method for monitoring the progression of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
  - (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
  - (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
  - (d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.
63. A method according to claim 62, wherein the binding agent is an antibody.
64. A method according to claim 63, wherein the antibody is a monoclonal antibody.
65. A method according to claim 62, wherein the cancer is a prostate cancer.
66. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
  - (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

67. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

68. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

69. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

70. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

71. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

72. A diagnostic kit, comprising:

- (a) one or more antibodies according to claim 21; and
- (b) a detection reagent comprising a reporter group.

73. A kit according to claim 72, wherein the antibodies are immobilized on a solid support.

74. A kit according to claim 73, wherein the solid support comprises nitrocellulose, latex or a plastic material.

75. A kit according to claim 72, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

76. A kit according to claim 72, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

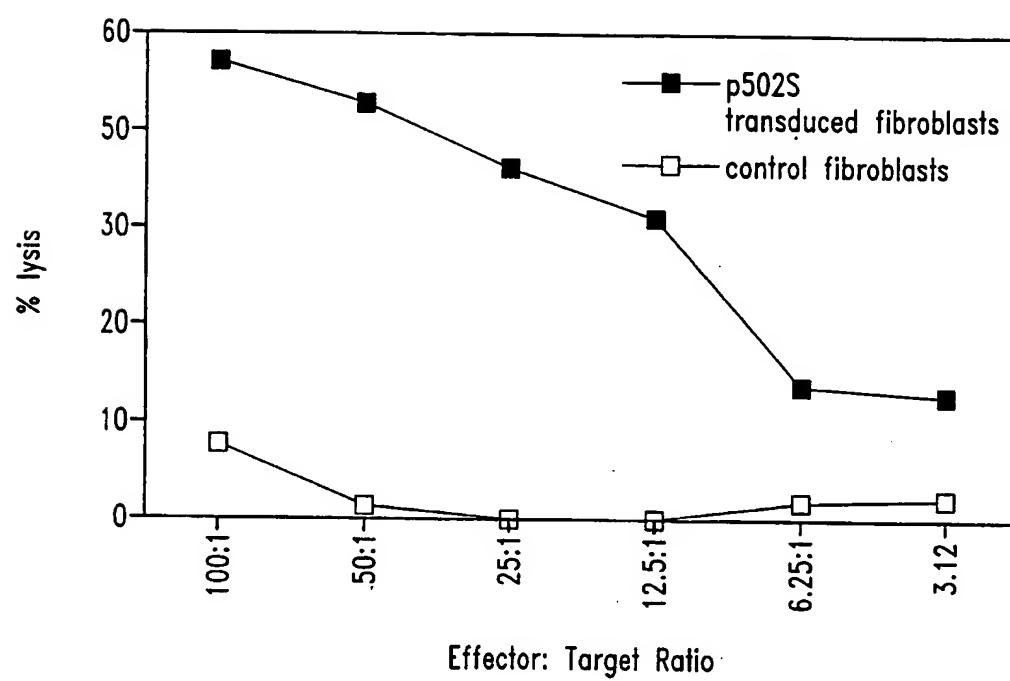
77. An oligonucleotide comprising 10 to 40 nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotides.

78. A oligonucleotide according to claim 77, wherein the oligonucleotide comprises 10-40 nucleotides recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

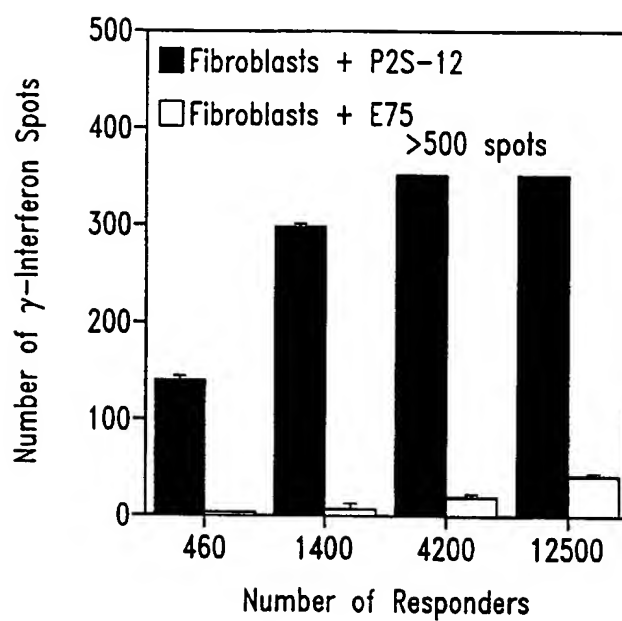
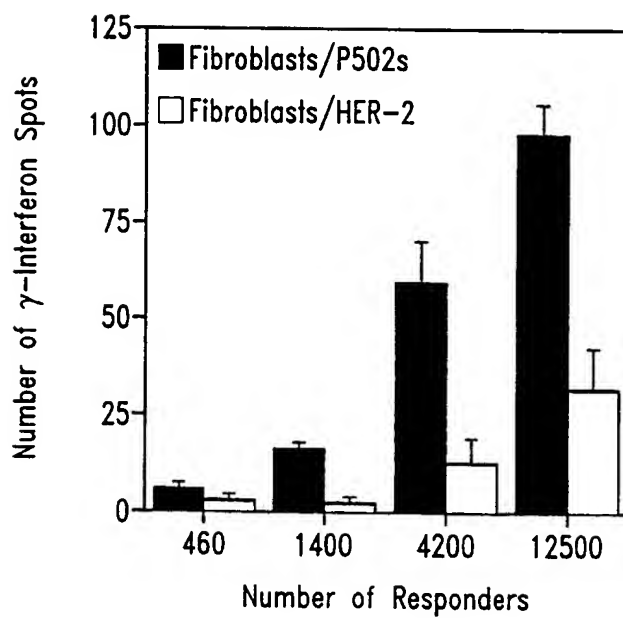
79. A diagnostic kit, comprising:

- (a) an oligonucleotide according to claim 77; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

1/5

*Fig. 1*

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*Fig. 2A**Fig. 2B*

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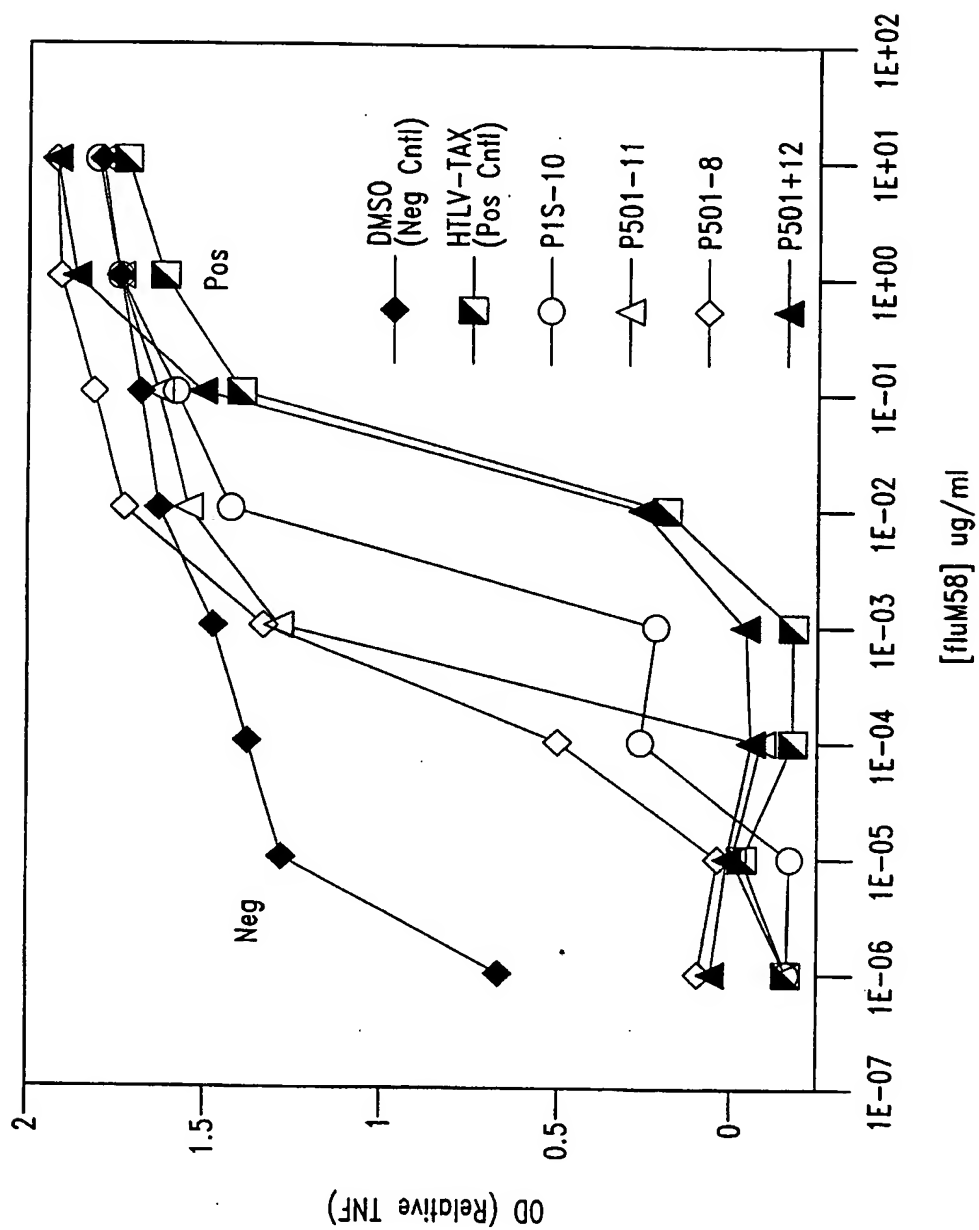
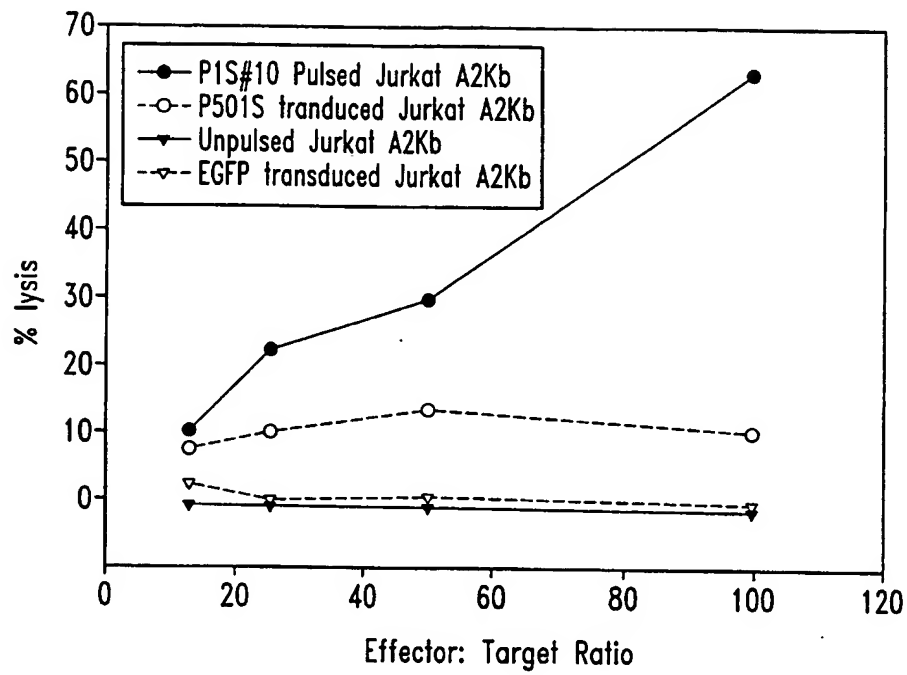
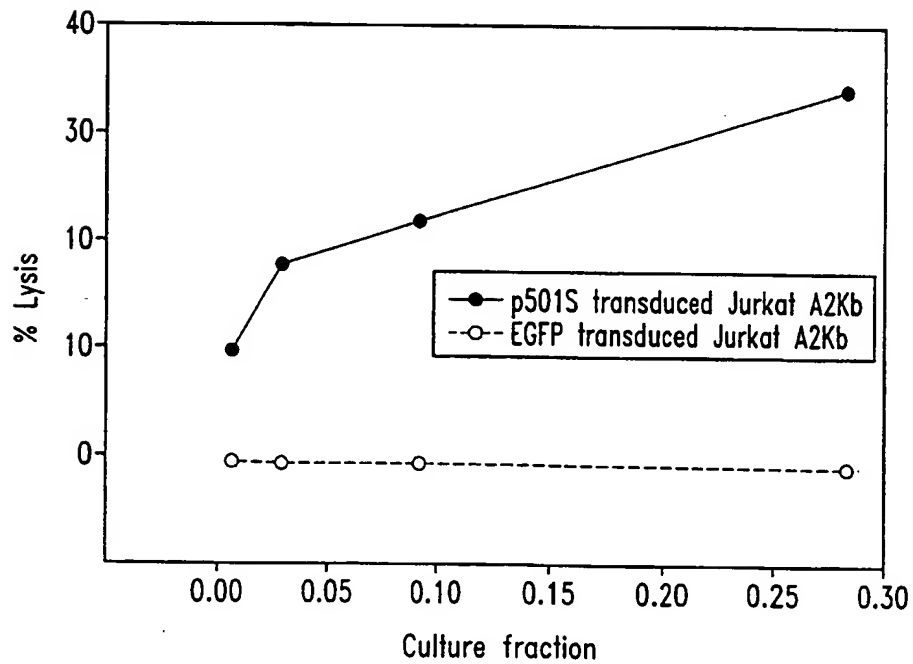


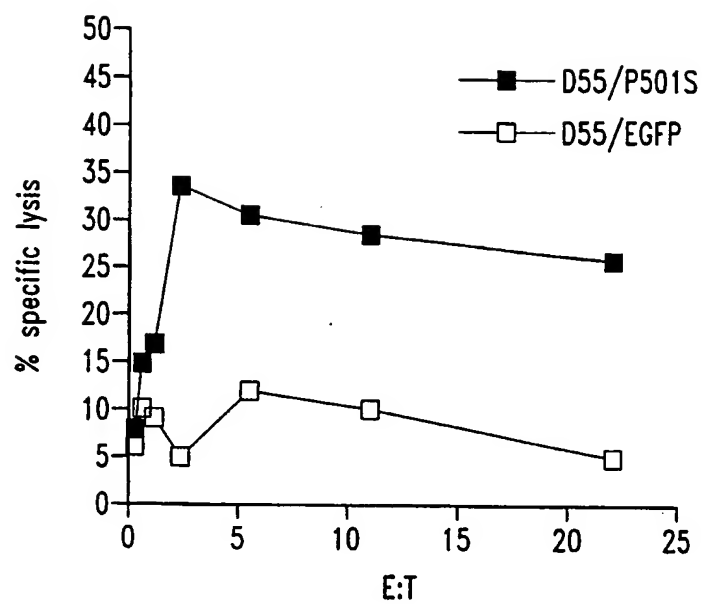
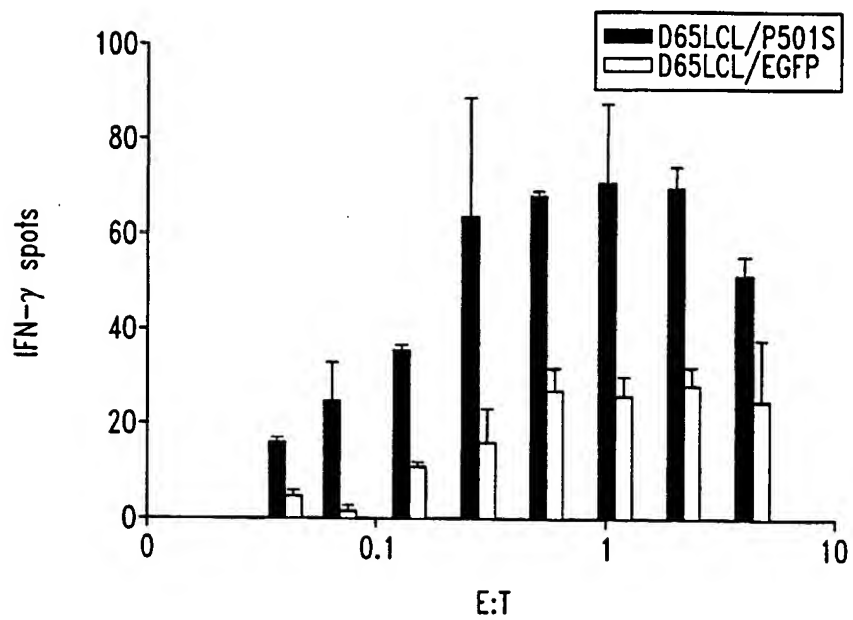
Fig. 3



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*Fig. 4**Fig. 5*

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*Fig. 6**Fig. 7*

## SEQUENCE LISTING

&lt;110&gt; Corixa Corporation

<120> COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
OF PROSTATE CANCER AND METHODS FOR THEIR USE

&lt;130&gt; 210121.42701PC

&lt;140&gt; PCT

&lt;141&gt; 1999-07-08

&lt;160&gt; 472

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 814

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (814)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1

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atcaaactcg	agggttgtct	ggaggacttc	aatacacctc	cccccatagt	gaatcagctt	120
ccaggggggc	cagtcctctc	ccttacttca	tccccatccc	atgccaaagg	aagaccctcc	180
ctccttggct	cacagccttc	tctaggcttc	ccagtgcctc	caggacagag	tgggttatgt	240
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tgccagctgc	attaatgaat	cgccaacgc	ncggggaaaa	gcggtttgcg	ttttgggggc	660
tcttcgcgtt	ctcgtcact	nantcctgcg	ctcggtcntt	cggctgcggg	gaacggtatc	720
actcctcaaa	ggnggtatta	cggttatccn	naaatcnggg	gatacccngg	aaaaaanttt	780
aacaaaaggg	cancaaaggg	cngaaacgta	aaaa			814

&lt;210&gt; 2

&lt;211&gt; 816

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (816)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 2

acagaaatgt	tggatggtgg	agcacctttc	tatacgactt	acaggacagc	agatggggaa	60
ttcatggctg	ttggagcaat	agaacccccag	ttctacgagc	tgctgatcaa	aggacttggg	120

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ctaaagtctg atgaacttcc caatcagatg agcatggatg attggccaga aatgaagaag      180
aagtttgtag atgtatttgc aaagaagacg aaggcagagt ggtgtcaa atttgacggc      240
acagatgcct gtgtgactcc ggttctgact tttgaggagg ttgttcatca tgatcacaac      300
aaggaacggg gctcgtttat caccagttag gagcaggacg tgagcccccg ccctgcacct      360
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gccgccaccg cgggtggagct ccagcttttg ttccctttag tgaggggttaa ttgcgcgctt      480
ggcgtaatac tgggtcatagc tgtttcctgt gtgaaattgt tatccgctca caattccccc      540
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cattaattgc gttgcgctca ctgcccgtt tccagtcggg aaaactgtcg tgccactgcn      660
ttantgaatc ngccaccccc cgggaaaagg cggttgcntt ttgggcctct tccgctttcc      720
tcgctcattg atcctngcnc ccggtcttcg gctgcggnga acggttcact cctcaaaggc      780
ggtntnccgg ttatcccaa acnggggata cccnga                                     816

```

&lt;210&gt; 3

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(773)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 3

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cttttgaaag aagggtggtc tgggggtgtt aacagcagag gtgcagggcg ggggctcacg      60
tcttgctcct cactggtgat aaacgagccc cgttccttgt tgtgatcatg atgaacaacc      120
tcttcaaaag tcagaaccgg agtcacacag gcattctgtc cgtcaaagat ttgacaccac      180
tctgccttcg tcttctttgc aaatacatct gcaaacttct tcttcatttc tggccaatca      240
tccatgctca tctgattggg aagttcatca gacttttagt canntccttt gatcagcagc      300
tcgtagaact ggggttctat tgctccaaca gccatgaatt ccccatctgc tgcctgttaa      360
gtcgtataga aagggtgctc accatccaac atgttctgtc ctgcaggggg ggcccgggtac      420
ccaattcgcc ctatantgag tcgtattacg cgcgctcact ggccgctcgt ttacaacgct      480
gtgactggga aaaccctggg cgttaccaac ttaatcgctc tgcagcacat ccccttttcg      540
ccagctgggc gtaatanaga aaaggcccg cccgatcgcc cttccaacag ttgcgcacct      600
gaatgggnaa atgggacccc cctgttaccg cgcattnaac ccccgngggg tttngttgtt      660
acccccacnt nnaccgctta cactttgcca gcgccttanc gcccgctccc tttcnccttt      720
cttcccttcc tttcncncn ctttcccccg ggggtttcccc cntcaaacc cna                                     773

```

&lt;210&gt; 4

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(828)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 4

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cctcctgagt cctactgacc tgtgctttct ggtgtggagt ccagggtgc taggaaaagg      60
aatgggcaga cacaggtgta tgccaatgtt tctgaaatgg gtataatttc gtcctctcct      120
tcggaacact ggctgtctct gaagacttct cgctcagttt cagtgaggac acacacaaag      180
acgtgggtga ccatgttgtt tgtgggtgac agagatggga ggggtggggc ccaccctgga      240
agagtggaca gtgacacaag gtggacactc tctacagatc actgaggata agctggagcc      300
acaatgcatg aggcacacac acagcaagga tgacnctgta aacatagccc acgctgtcct      360

```

```

gnngggcactg ggaagcctan atnaggccgt gagcanaaag aaggggagga tccactagtt      420
ctanagcggc  cgccaccgcg gtgganctcc ancttttggt cccttttagtg aggggttaatt      480
gcgcgcttg  cntaatcatg gtcatanctn tttcctgtgt gaaattgtta tccgctcaca      540
attccacaca acatacganc cggaacata aantgtaaac ctgggggtgcc taatgantga      600
ctaactcaca ttaattgcgt tgcgctcact gcccgcttcc caatcnggaa acctgtcttg      660
ccncttgcat tnatgaatcn gccaaacccc ggggaaaagc gtttgcggtt tgggcgctct      720
tccgcttcct cnctcantta ntccctncnc tcgggtcatc cggtgcngc aaaccgggtc      780
accnctcca  aagggggtat tccggtttcc ccnaatccgg gganancc      828

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&lt;210&gt; 5

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(834)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 5

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tttttttttt tttttactga tagatggaat ttattaagct tttcacatgt gatagcacat      60
agttttaatt gcatccaaag tactaacaaa aactctagca atcaagaatg gcagcatggt      120
attttataac aatcaacacc tgtggctttt aaaatttggt tttcataaga taatttatac      180
tgaagtaa atagccatgc ttttaaaaaa tgcttttaggt cactccaagc ttggcagtta      240
acatttgga taaacaataa taaaacaatc acaatttaat aaataacaaa tacaacattg      300
taggccataa tcatatacag tataaggaaa aggtggtagt gttgagtaag cagttattag      360
aatagaatac cttggcctct atgcaaatat gtctagacac tttgattcac tcagccctga      420
cattcagttt tcaaagtagg agacagggtc tacagtatca ttttacagtt tccaacacat      480
tgaaaacaag tagaaaatga tgagttgatt ttatttaatg cattacatcc tcaagagtta      540
tcaccaaccc ctcagttata aaaaattttc aagttatatt agtcatataa cttggtgtgc      600
ttatttttaa ttagtgctaa atggattaag tgaagacaac aatgggtccc taatgtgatt      660
gatattggtc atttttacca gcttctaaat ctnaactttc aggcctttga actggaacat      720
tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa      780
tgttattttg ttaaaaatta aattttaacc tgggtggaaa ataatttgaa atna      834

```

&lt;210&gt; 6

&lt;211&gt; 818

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(818)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 6

```

tttttttttt tttttttttt aagaccctca tcaatagatg gagacataca gaaatagtca      60
aaccacatct acaaaatgcc agtatcaggc ggcggcttcg aagccaaagt gatgtttgga      120
tgtaaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagttg agccaataat      180
gacgtgaagt ccgtggaagc ctgtggctac aaaaaatggt gagccgtaga tgccgtcgga      240
aatgggtgaag ggagactcga agtactctga ggcttgtagg agggtaaaat agagaccag      300
taaaattgta ataagcagtg cttgaattat ttggtttcgg ttgttttcta ttagactatg      360
gtgagctcag gtgattgata ctctgatgc gagtaatacg gatgtgttta ggagtgggac      420
ttctagggga tttagcgggg tgatgcctgt tggggggccag tgccctccta gttggggggg      480
aggggctagg ctggagtggg aaaaggctca gaaaaatcct gcgaagaaaa aaacttctga      540

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ggtaataaat aggattatcc cgtatcgaag gccttttttg acaggtggtg tgtggtggcc 600
ttggtatgtg ctttctcgtg ttacatcgcg ccatcattgg tatatgggta gtgtgttggg 660
ttantanggc ctantatgaa gaacttttgg antggaatta aatcaatngc ttggccggaa 720
gtcattanga nggctnaaaa ggccctgtta ngggtctggg ctnggtttta cccnaccat 780
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<210> 7

<211> 817

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(817)

<223> n = A,T,C or G

<400> 7

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ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gtagcgggta 180
aagtggtttg gtttagacgt ccgggaattg catctgtttt taagccta atgtggggacag 240
ctcatgagtg caagacgtct tgtgatgtaa ttattatacn aatgggggct tcaatcggga 300
gtactactcg attgtcaacg tcaaggagtc gcaggtcgcc tgggtctagg aataatgggg 360
gaagtatgta ggaattgaag attaatccgc cgtagtcggt gttctcctag gttcaatacc 420
attggtggcc aattgatttg atggtaaggg gagggatcgt tgaactcgtc tgttatgtaa 480
aggatncctt ngggatggga aggcnatnaa ggactangga tnaatggcgg gcangatatt 540
tcaaacngtc tctanttcct gaaacgtctg aaatgttaat aanaattaan tttngttatt 600
gaatnttnng gaaaagggtc tacaggacta gaaaccaa atngaaaanta atnntaangg 660
cnttatcntn aaaggtnata accnctccta tnatcccacc caatngnatt cccacnncnn 720
acnattggat nccccanttc canaaanggc cccccccgg tgnannccnc cttttgttcc 780
cttnantgan ggttattcnc cctngcntt atcanc 817

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<210> 8

<211> 799

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(799)

<223> n = A,T,C or G

<400> 8

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cataaggaga actttctgct ggcacgcgct agggacaagc gggagagcga ctccgagcgt 120
ctgaagcgca cgtcccagaa ggtggacttg gcaactgaaac agctgggaca catccgcgag 180
tacgaacagc gcctgaaagt gctggagcgg gaggtccagc agtgtagccg cgtcctgggg 240
tggtggccg angcctganc cgctctgcct tgctgcccc angtgggccg ccacccctg 300
acctgcctgg gtccaaacac tgagccctgc tggcggactt caagganaac cccacangg 360
ggattttgct cctanantaa ggctcatctg ggccctcgcc cccccacctg gttggccttg 420
tctttgagt gagccccatg tccatctggg ccaactgtcng gaccacctt ngggagtgtt 480
ctccttaca ccaannatg cccggctcct cccggaaacc antccancc tnggaaggat 540
caagnccnnt atccactnnt nctanaaccg gccnccncc cngtggaacc nccttntgt 600
tcttttctn tnaagggttaa tnnccgcttg gccttnccan ngctctncc nttttccnnt 660
gttnaaattg ttangcnccc nccnntccn cennnnnnan cccgaccnnc annttnnann 720

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ncctgggggt nccnncngat tgaccnnc nccctntant tgcnttnggg ncnntgccc 780  
ctttccctct nggganncg 799

<210> 9

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 9

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caaggacaag	gccaccaggt	gcgggggccc	aagccacat	gacccctact	ctatgagcaa	180
aatccccctgt	gggggcttct	ccttgaagtc	cgccancagg	gctcagtctt	tggacccang	240
cagggtcatgg	ggttgtngnc	caactggggg	ccncaacgca	aaanggcnca	gggcctcngn	300
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ttcntacccg	cgnatntgtc	ccanctgttt	cngtgccnac	tccancttct	nggacgtgcg	420
ctacatacgc	ccggantcnc	nctcccgtt	tgtccctatc	cacgtncan	caacaaattt	480
cncctantg	caccnatcc	cacntttnc	agntttccnc	nncgngcttc	cttntaaaag	540
ggttganccc	cggaaaatnc	cccaaagggg	gggggccngg	tacccaactn	ccccctnata	600
gctgaantcc	ccatnaccnn	gnctcnatgg	ancntccnt	tttaannacn	ttctnaactt	660
gggaananc	ctcgncentn	ccccnttaa	tccnccttg	cnangnncnt	ccccnntcc	720
ncccnmntng	gcntntnann	cnaaaaaggc	ccnnnancaa	tctcctnncn	cctcanttcg	780
ccanccctcg	aaatcggccn	c				801

<210> 10

<211> 789

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(789)

<223> n = A,T,C or G

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agatcctgcc	ctacacactg	gcctccctct	accaccggga	gaagcagggtg	ttcctgcca	180
aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	cctgatgacc	agcttcctgc	240
caggccctaa	gcctggagct	ccctcccta	atggacacgt	gggtgctgga	ggcagtggcc	300
tgtcccccacc	tccaccgcg	ctctgcgggg	cctctgcctg	tgatgtctcc	gtacgtgtgg	360
tggtgggtga	gcccaccgan	gccagggtgg	ttccgggccc	gggcatctgc	ctggacctcg	420
ccatcctgga	tagtgcttcc	tgctgtccca	ngtggcccca	tccctgttta	tgggctccat	480
tgtccagctc	agccagtctg	tactgccta	tatggtgtct	gccgcaggcc	tgggtctggt	540
ccatttact	ttgctacaca	ggtantattt	gacaagaacg	anttggccaa	atactcagcg	600
ttaaaaaatt	ccagcaacat	tgggggtgga	aggcctgcct	caactgggtcc	aactccccgc	660
tcctgttaac	cccatggggc	tgccggcttg	gccgccaatt	tctgtgtctg	ccaaantnat	720
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<210> 11  
 <211> 772  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(772)  
 <223> n = A,T,C or G

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 accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180  
 tgtgggctga ggggacctg ttcttgtgtg ttgccctca ggactcttcc cctacaaata 240  
 actttcatat gttcaaattcc catggaggag tgtttcatcc tagaaactcc catgcaagag 300  
 ctacattaaa cgaagctgca ggtaagggg cttanagatg ggaaaccagg tgactgagtt 360  
 tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420  
 ctgagcctgg gtaatccacc tgcagagtc ccgcattcca gtgcatggaa ccttctggc 480  
 ctccctgtat aagtccagac tgaaccccc ttggaaggnc tccagtcagg cagccctana 540  
 aactggggaa aaaagaaaag gacgccccan ccccagctg tgcantacg cacctcaaca 600  
 gcacaggggtg gcagcaaaaa aaccacttta ctttggcaca acaaaaaact ngggggggca 660  
 accccggcac cccnangggg gttaacagga ancngggnaa cntggaaccc aattnaggca 720  
 ggcccnccac cccnaatntt gctgggaaat ttttctccc ctaaattntt tc 772

<210> 12  
 <211> 751  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(751)  
 <223> n = A,T,C or G

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 ttggctgtgt tgggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180  
 aagtanggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc 240  
 atggtggtgt tccacacttg agtgaagtct tcttgggaac cataatcttt cttgatggca 300  
 ggcactacca gcaacgtcag ggaagtgtc agccattgtg gtgtacacca aggcgaccac 360  
 agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc 420  
 acacttgctc tcagtcttan caccatanca gccntgaaa accaananca aagaccacna 480  
 cncgggctgc gatgaagaaa tnacccncg ttgacaaact tgcatggcac tggganccac 540  
 agtggcccn aaaaatcttca aaaaggatgc cccatcnatt gacccccaa atgcccactg 600  
 ccaacagggg ctgccccacn cncnnaacga tganccnatt gnacaagatc tncntggtct 660  
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<210> 13  
 <211> 729  
 <212> DNA  
 <213> Homo sapien



<220>  
 <221> misc\_feature  
 <222> (1)...(729)  
 <223> n = A,T,C or G

<400> 13  
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 accatgcagt gcttcagctt cattaagacc atgatgatcc tcttcaattt gctcatcttt 180  
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 ctcacgcag ccggcggtgt ggtcttagct ctagggttcc tgggctgcta tgggtgctaag 360  
 actgagagca agtgtgccct cgtgacgttc ttcttcaccc tcctcctcat cttcattgct 420  
 gaggttgcaa tgctgtggtc gccttggtgt acaccacaat ggctgagcac tcctgacgt 480  
 tgctggtaat gcctgccatc aanaaaagat tatgggttcc caggaanact tcactcaagt 540  
 gttggaacac caccatgaaa gggctcaagt gctgtggctt cnnccaacta tacggatttt 600  
 gaagantcac ctacttcaaa gaaaanagtg cctttccccc atttctgttg caattgacaa 660  
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 attnaaggg 729

<210> 14  
 <211> 816  
 <212> DNA  
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<220>  
 <221> misc\_feature  
 <222> (1)...(816)  
 <223> n = A,T,C or G

<400> 14  
 tgctcttcct caaagttggt cttgttgcca taacaaccac cataggtaaa gcgggcgcag 60  
 tgttcgctga aggggttgta gtaccagcgc gggatgctct ccttgcagag tcctgtgtct 120  
 ggcaggtcca cgcagtgcc tttgtcactg gggaaatgga tgcgctggag ctctgcaaag 180  
 ccactcgtgt atttttcaca ggcagcctcg tccgacgcgt cggggcagtt gggggtgtct 240  
 tcacactcca ggaaactgtc natgcagcag ccattgctgc agcggaaactg ggtgggctga 300  
 cangtgccag agcacactgg atggcgctt tccatgnnan gggccctgng ggaaagtccc 360  
 tgancccan anctgctct caaangcccc accttgaca ccccgacagg ctagaatgga 420  
 atcttcttcc cgaaaggtag ttnttcttgt tgcccaancc anccccntaa acaaactctt 480  
 gcanatctgc tccgnggggg tcntantacc ancgtgggaa aagaacccca ggcngcgaac 540  
 caancttggt tggatncaa gcnataatct nctnttctgc ttggtggaca gcaccantna 600  
 ctgtnnanct ttagncctg gtcctcntgg gttgnncttg aacctaatcn ccnntcaact 660  
 gggacaaggt aantngcct cctttnaatt ccnancntn cccctggtt tggggttttn 720  
 cncnctccta cccagaaan nccgtgttcc cccccaacta ggggccnaaa ccnntnttcc 780  
 cacaacctn cccacccac ggggtcngnt gggtng 816

<210> 15  
 <211> 783  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(783)  
 <223> n = A,T,C or G

```

<400> 15
ccaaggcctg ggcaggcata nacttgaagg tacaacccca ggaaccctg gtgctgaagg      60
atgtggaaaa cacagattgg cgcctactgc ggggtgacac ggatgtcagg gtagagagga      120
aagacccaaa ccaggtggaa ctgtggggac tcaaggaang cacctacctg ttccagctga      180
cagtgcactag ctcagaccac ccagaggaca cggccaacgt cacagtcact gtgctgtcca      240
ccaagcagac agaagactac tgcctcgcac ccaacaangt gggtcgctgc cggggctctt      300
tcccacgctg gtactatgac cccacggagc agatctgcaa gagtttcgtt .tatggaggct      360
gcttgggcaa caagaacaac taccttcggg aagaagagtg cattctancc tgtcnggggtg      420
tgcaagggtg gcctttgana ngcanctctg gggctcangc gactttcccc cagggccctt      480
ccatggaaag gcgccatcca ntgttctctg gcacctgtca gcccaccag ttccgctgca      540
ncaatggctg ctgcatcnac antttcctng aattgtgaca acacccccca ntgcccccaa      600
ccctcccaac aaagcttccc tgttnaaaaa .tacnccantt ggcttttnac aaacncccg      660
cncctccttt ttccccnntn aacaaagggc nctngcnttt gaactgcccn aaccnnggaa      720
tctnccnngg aaaaantncc cccctgggtt cctnnaancc cctccnnaa anctncccc      780
ccc

```

```

<210> 16
<211> 801
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(801)
<223> n = A,T,C or G

```

```

<400> 16
gccccaatc cagctgccac accaccacg gtgactgcat tagttcggat gtcatacaaa      60
agctgattga agcaaccctc tactttttgg tcgtgagcct tttgcttggg gcaggtttca      120
ttggctgtgt tggtagcgtt gtcatgcaa cagaatgggg gaaaggcact gttctctttg      180
aagtaggggt agtcctcaaa atccgtatag ttgggtgaagc cacagcactt gagccctttc      240
atgggtgggtg tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca      300
ggcactacca gcaacgtcag gaagtgtcga gccattgtgg tgtacaccaa ggcgaccaca      360
gcagctgcaa cctcagcaat gaagatgagg aggaggatga agaagaacgt cncgagggca      420
cacttgctct cgtcttagc accatagcag cccangaaac caagagcaaa gaccacaacg      480
ccngctgcga atgaaagaaa ntaccacagt tgacaaactg catggccact ggacgacagt      540
tggcccgaan atcttcagaa aagggatgcc ccacgattg aacaccana tgcccactgc      600
cnacaggggt gcncncncn gaaagaatga gccattgaag aaggatcntc ntggtcttaa      660
tgaactgaaa ccntgcatgg tggccctgt tcagggtctt tggcagtga ttctganaaa      720
aaggaacngc ntnagcccc ccaaangana aaacaccccc gggtgttgcc ctgaattggc      780
ggccaaggan ccctgccccn g

```

```

<210> 17
<211> 740
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(740)
<223> n = A,T,C or G

```

```

<400> 17
gtgagagcca ggcgtccctc tgcctgccca ctcaaggga acacccggga gctgttttgt      60

```

cctttgtgga	gcctcagcag	ttccctcttt	cagaactcac	tgccaagagc	cctgaacagg	120
agccaccatg	cagtgtttca	gcttcattaa	gaccatgatg	atcctcttca	atttgctcat	180
ctttctgtgt	ggtgcagccc	tggtggcagt	gggcatctgg	gtgtcaatcg	atggggcatc	240
ctttctgaag	atcttcgggc	cactgtcgtc	cagtgccatg	cagtttgtca	acgtgggcta	300
cttcctcatc	gcagccggcg	ttgtggtctt	tgctcttggt	ttcctgggct	gctatggtgc	360
taagacggag	agcaagtgtg	ccctcgtgac	gttcttcttc	atcctcctcc	tcattctcat	420
tgctgaagtt	gcagctgctg	tggtcgcctt	ggtgtacacc	acaatggctg	aaccattcct	480
gacgttgctg	gtantgcctg	ccatcaanaa	agattatggg	ttcccaggaa	aaattcactc	540
aantntggaa	caccnccatg	aaaagggctc	caatttctgn	tggtctcccc	aactataccg	600
gaattttgaa	agantcncct	tacttccaaa	aaaaaanant	tgcttttnc	ccnttctgt	660
tgcaatgaaa	acntcccaan	acngccaatn	aaaacctgcc	cnnncaaaaa	ggntcncaaa	720
caaaaaaant	nnaagggttn					740

&lt;210&gt; 18

&lt;211&gt; 802

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(802)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 18

ccgctggttg	cgctgggtcca	gngnagccac	gaagcacgtc	agcatcacaca	gcctcaatca	60
caaggtcttc	cagctgccgc	acattacgca	gggcaagagc	ctccagcaac	actgcatatg	120
ggatacactt	tacttttagca	gccaggggtga	caactgagag	gtgtcgaagc	ttattcttct	180
gagcctctgt	tagtggagga	agattccggg	cttcagctaa	gtagtacgag	tatgtcccat	240
aagcaaacac	tgtgagcagc	cggaaggtag	aggcaaatgc	actctcagcc	agctctctaa	300
cattgggcat	gtccagcagt	tctccaaaca	cgtagacacc	agnggcctcc	agcacctgat	360
ggatgagtgt	ggccagcgct	gcccccttgg	ccgacttggc	taggagcaga	aattgctcct	420
ggttctgccc	tgtcaccttc	acttcgcgac	tcactactgc	actgagtgtg	ggggacttgg	480
gctcaggatg	tccagagacg	tggttccgcc	ccctcncctt	atgacaccgn	ccanncaacc	540
gtcggctccc	gccgantgng	ttcgtcgtnc	ctgggtcagg	gtctgctggc	cnctacttgc	600
aanttcgtc	nggccccatg	aattcaccnc	accggaactn	gtangatcca	ctnnttctat	660
aaccgngcgc	caccgcnnt	ggaactccac	tcttnttnc	tttacttgag	ggtaagggtc	720
acccttnncg	ttaccttggg	ccaaaccntn	ccntgtgtcg	anatngtnaa	tcnggncna	780
tnccancnc	atangaagcc	ng				802

&lt;210&gt; 19

&lt;211&gt; 731

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(731)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 19

cnaagcttcc	aggtnacggg	ccgcnaancc	tgacccnagg	tancanaang	cagnncgagg	60
gagcccaccg	tcacngggng	gngtctttat	nggagggggc	ggagccacat	cnctggacnt	120
cntgacccca	actcccncc	ncncantgca	gtgatgagtg	cagaactgaa	ggtnacgtgg	180
caggaaccaa	gancaaannc	tgctccnntc	caagtccgcn	nagggggcgg	ggctggccac	240
gcncatccnt	cnagtgtctg	aaagccccnn	cctgtctact	tggttgagga	acngcnnga	300

catgcccagn	gttanataac	nggcngagag	tnantttgcc	tctcccttcc	ggctgcgean	360
cngntntgct	tagnggacat	aacctgacta	cttaactgaa	ccnngaate	tnccnccct	420
ccactaagct	cagaacaaaa	aacttcgaca	ccactcantt	gtcacctgnc	tgctcaagta	480
aagtgtaccc	catncccaat	gtntgctnga	ngetctgncc	tgcnttangt	tcggtcctgg	540
gaagacctat	caattnaagc	tatgtttctg	actgcctctt	gctccctgna	acaancnacc	600
cnncnntcca	agggggggnc	ggcccccaat	ccccccaacc	ntnaattnan	tttancccn	660
ccccngggcc	cgcccttcta	cnancntcnn	nnacngggna	aaaccnnngc	tttncccaac	720
nnaatcncct	t					731

&lt;210&gt; 20

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(754)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 20

tttttttttt	tttttttttt	taaaaacccc	ctccattnaa	tgnaaaacttc	cgaaattgtc	60
caacccccctc	ntccaaatnn	ccntttccgg	gnggggggttc	caaacccean	ttanntttgg	120
annttaaatt	aaatnttnt	tgngggnnna	ancnnaatgt	nangaaagtt	naaccanta	180
tnantctnaa	tncttgaaa	ccngtngntt	ccaaaaatnt	ttaaccctta	antccctccg	240
aatngttna	nggaaaaccc	aantttctnt	aagggtgttt	gaaggntnaa	tnaaaanccc	300
nnccaattgt	tttngccac	gcctgaatta	attggnntcc	gntgttttcc	nttaaaanaa	360
ggnnancccc	ggttantnaa	tccccccnnc	cccaattata	ccganttttt	ttngaattgg	420
ganccncgg	gaattaacgg	ggnnntccc	tnttgggggg	cnggnncccc	ccccntcggg	480
ggttngggnc	aggnccnaat	tgtttaagg	tccgaaaaat	ccctccnaga	aaaaaanctc	540
ccaggntgag	nntnggggtt	ncccccccc	cangggccct	ctcgnaagtt	tggggtttgg	600
ggggcctggg	attttntttc	ccctnttnc	tcccccccc	ccnggganag	agggttngngt	660
ttgtntcnc	ggccccnccn	aaganccttn	ccganttnan	ttaaatccnt	gcctnggcga	720
agtcnntgn	agggntaaan	ggccccctnn	cggg			754

&lt;210&gt; 21

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(755)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 21

atcancccat	gacccnaac	nngggaccnc	tcancgggnc	nnncnaccnc	cggecnatca	60
nngtnagnnc	actncnnttn	natcacnccc	cncnactac	gccncnanc	cnacgcncta	120
nncanatncc	actganngcg	cgangtngan	ngagaaanct	nataccanag	ncaccanacn	180
ccagctgtcc	nanaangcct	nnnatacngg	nnnatccaat	ntgnancctc	cnaagtattn	240
nncnncanat	gattttcctn	ancegattac	ccntncccc	tanccctcc	cccccaacna	300
cgaaggcnct	ggncnaagg	nngcgnccnc	ccgctagntc	cccncaagt	cnencnecta	360
aactcancn	nattacncgc	ttcntgagta	tactccccg	aatctcaccc	tactcaactc	420
aaaaanatan	gatacaaaat	aatncaagcc	tgnttatnac	actntgactg	ggtctctatt	480
ttagnngtcc	ntnaancntc	ctaatacttc	cagtctncct	tcnccaattt	ccnaanggct	540
ctttcngaca	gcantttttg	gttcccnntt	gggttcttan	ngaattgcc	ttcntngaac	600

gggctcttct	tttccttcgg	ttancctggn	ttcnnccggc	cagttattat	ttcccntttt	660
aaattcttnc	cntttanttt	tggcnttcna	aacccccggc	cttgaaaacg	gccccctggt	720
aaaaggttgt	tttganaaaa	tttttgtttt	gttcc			755

&lt;210&gt; 22

&lt;211&gt; 849

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(849)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 22

tttttttttt	tttttangtg	tngtcgtgca	ggtagaggct	tactacaant	gtgaanacgt	60
acgctnggan	taangcgacc	cgantttctag	ganncnccct	aaaatcanac	tgtgaagatn	120
atcctgnnna	cggaanggtc	accggnngat	nntgctaggg	tgncnctcc	cannncnttn	180
cataactcng	nggccctgcc	caccaccttc	ggcgccccng	ngnccgggcc	cgggtcattn	240
gnnttaaccn	cactnngcna	ncggtttccn	ncccnncng	accnnggcga	tccggggtnc	300
tctgtcttcc	cctgnagncn	anaaantggg	ccncggncce	ctttaccct	nnacaagcca	360
cngcentcta	ncnengccc	ccccctcant	nngggggact	gccnanngt	ccgttntctng	420
nnaccccnnn	gggtncctcg	gttgtegant	cnaccgnang	ccanggatc	cnaaggaagg	480
tgcgttnttg	gcccctaccc	ttcgtncgg	nnacaccttc	ccgacnanga	nccgctcccg	540
cncnncgng	cctcncctcg	caacacccgc	nctcntngt	ncggnnnccc	ccccacccgc	600
nccctcncnc	ngnncgnancn	ctcncncnc	gtctcannca	ccaccccgcc	ccgccaggcc	660
ntcanccacn	ggngnacnng	nagcncnttc	gcnccgcgcn	gcgncncct	cgccncngaa	720
ctnctcngg	ccantnncgc	tcaancenna	cnaaacgcgc	ctgcgcggcc	cgnagcgnc	780
ncctcncga	gtcctcccg	cttcnacc	angnttccn	cgaggacacn	nnaccccgcc	840
nncangcgg						849

&lt;210&gt; 23

&lt;211&gt; 872

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(872)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 23

gcgcaaaacta	tacttcgctc	gnactcgtgc	gcctcgtcnc	tcttttcttc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatcnan	aagntcganc	agtccaaact	gantaacaca	120
cacacncnan	aganaaatcc	nctgccttcc	anagtanaen	attgaacnng	agaaccangc	180
nggcgaatcg	taatnaggcg	tgcgcgcga	atntgtcncc	gtttattntn	ccagcntcnc	240
ctnccnacc	tacntcttcn	nagctgtcnn	acccctngtn	cgnaccccc	naggctcgga	300
tgcgggtttn	nntgaccgng	cnccccctcc	ccccctccat	nacganccnc	ccgcaccacc	360
nanngcncgc	nccccgnct	cttcgcnc	ctgtcctntn	cccctgtngc	ctggcncngn	420
accgcattga	ccctcgcenn	ctncnngaaa	ncgnanacgt	ccgggttggn	annancgctg	480
tgggnnngcg	tctgncccgc	gttccctccn	ncncttcca	ccatcttct	tacnggggtc	540
ccnccgcntc	tcnnncacnc	cctgggaagc	tnctcctngc	cccccttnac	tccccccctt	600
cgncgtgncc	cgnccccacc	ntcatttnca	naegntcttc	acaannncct	ggntnnctcc	660
cnancngncn	gtcanccnag	ggaagggngg	ggnnccnntg	nttgacgttg	nggngangtc	720
cgaanantcc	tcnccntcan	cncctaccct	cgggcgnnct	ctcngttnc	aacttancaa	780

ntctcccccg ngngcncntc tcagcctenc ccnccccnct ctctgcantg tncctctgctc 840  
tnaccnntac gantnttcgn cncctctttt cc 872

<210> 24

<211> 815

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(815)

<223> n = A,T,C or G

<400> 24

gcatgcaagc ttgagtattc tatagngtca cctaaatanc ttggcntaat catgggtcnta	60
nctgncttcc tgtgtcaaatt gtatacnaaa tanatatgaa tctnatntga caagannnga	120
tctnccatta gtaacaantg tntgtgccat cctgtcngan canattccca tnnattncgn	180
cgcattcncn gcncantatn taatngggaa ntcnnntnnn ncaccnncat ctatcntncc	240
gcnccttgac tggagagat ggatnattc tntntgacc nacatgttca tcttggattn	300
aananccccc cgcngnccac cggttngnng cnagcnnctc ccaagacctc ctgtggaggt	360
aacctgcgtc aganncatca aacntgggaa acccgcncc angtnnaagt ngnnncanan	420
gatcccgctc aggnntnacc atcccttenc agegccccct ttngtgccct anagnnagc	480
gtgtccnanc cncctaacat ganacgcgcc agnccanccg caattnggca caatgtcngc	540
gaaccccccta gggggantna tncaaanccc caggattgtc cncncangaa atcccnanc	600
ccnccctac ccnctttgg gacngtgacc aantcccgga gtncagtcg gccngnctc	660
ccccaccggt nncntgggg ggggtgaantc cngnntcanc cngncgaggn ntcgnaagga	720
accggnccn ggncgaanng ancntcnga agngcncnt cgtataaccc cccctcncca	780
nccnacngnt agntcccccc cngggtncgg aangg	815

<210> 25

<211> 775

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(775)

<223> n = A,T,C or G

<400> 25

ccgagatgtc tcgctccgtg gccttagctg tgctcgcgt actctctctt tctggcctgg	60
aggctatcca gcgtactcca aagattcagg tttactcacg tcatccagca gagaatggaa	120
agtcaaattt cctgaattgc tatgtgtctg ggtttcatcc atccgacatt gaanttgact	180
tactgaagaa tgganagaga attgaaaaag tggagcattc agacttgtct ttcagcaagg	240
actggtcttt ctatctctg tactacactg aattcacccc cactgaaaaa gatgagtatg	300
cctgcccgtg gaaccatgtg actttgtcac agcccaagat agttaagtgg gatcgagaca	360
tgtaagcagn cnnatggaa gtttgaagat gccgcatttg gattggatga attccaaatt	420
ctgcttgctt gcnttttaaat antgatatgc ntatacacc taccctttat gnccccaat	480
tgtaggggtt acatnantgt tcnctnnga catgatctc ctttataant ccnctntcg	540
aattgcccgt cncnngttn ngaatgtttc cnaaaccacg gttggctccc ccaggtcncc	600
tcttacggaa gggcctgggc cnccttncaa ggttggggga accnaaaatt tcnctntgc	660
ccnccncca cnccttgng nncncanttt ggaaccttc cnattccctc tggcctcnna	720
nccttnncta anaaaacttn aaancgtngc naaanntttn acttcccccc ttacc	775

<210> 26

<211> 820  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(820)  
 <223> n = A,T,C or G

<400> 26  
 anattantac agtghtaatct tttcccagag gtgtgtanag ggaacggggc ctagaggcat 60  
 cccanagata ncttatanca acagtgtctt gaccaagagc tgctgggcac atttcctgca 120  
 gaaaagggtg cgggtcccat cactcctcct ctcctatagc catcccagag ggggtgagtag 180  
 ccatcangcc ttcgggtggga gggagtcang gaaacaacan accacagagc anacagacca 240  
 ntgatgacca tgggcgggag cgagcctctt cctgnaccg ggggtggcana nganagccta 300  
 nctgagggggt cacactataa acgttaacga ccnagatnan cacctgttc aagtgcaccc 360  
 ttcctacctg acnaccagn accnnnaact gcngcctggg gacagcctg ggancagcta 420  
 acnnagcact cacctgcccc cccatggccg tncgctccc tggtcctgnc aagggaagct 480  
 cctgtgtgga attncgggga naccaaggga nccccctcct ccactgtga aggaaaaann 540  
 gatggaattt tnccttccg gccntcccc tcttcttta cagccccct nntactctc 600  
 tccctctntt ntcctgncnc acttttnacc ccnnnatttc ccttnattga tcggannctn 660  
 ganattccac tnnccctnc cntcnatcng naanacnaaa nactntctna ccnnggggat 720  
 gggnnccctg ntcactctct cttttctcct accnccnntt ctttgcctct ccttngatca  
 780tccaaccntc gntggcentn ccccccnntt tcttttcccc  
 820

<210> 27  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(818)  
 <223> n = A,T,C or G

<400> 27  
 tctgggtgat ggcctcttcc tctcagggga cctctgactg ctctgggcca aagaatctct 60  
 tgtttcttct ccgagcccca ggcagcgggtg attcagccct gcccaacctg attctgatga 120  
 ctgcggatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggaggggagc 180  
 ctgctgagca cttccgcccc tcacctgcc cagccctgc catgagctct gggtgggtc 240  
 tccgcctcca ggggttctgct ctccangca ngccancaag tggcgctggg ccacactggc 300  
 ttcttctgc cccntccctg gctctganc tctgtcttcc tgtcctgtgc angcncctg 360  
 gatctcagtt tccctcctc anngaactct gtttctgann tcttcantta actntgantt 420  
 tatnaccnan tggnetgtnc tgtcnactt taatgggcn gaccggctaa tccctccctc 480  
 nctcccttcc anttcnnna accngettnc cntctctcc ccntancccg ccngggaanc 540  
 ctctttgccc ctnaccang gccnnnaccg ccctnnctn ggggggcnng gtnnctncnc 600  
 ctgntnnccc cctcncnnt tncctgtcc cncnncnng nngcannttc ncngtcccn 660  
 tnnctctcn ngntnctgnaa ngntcncntn tnnnnngnnc ngntnnctnc tccctctcnc 720  
 cnnntgnang tnnntnnnc ncngncccc nnnnnnnnn nggnntnnn tctncncngc 780  
 cccnncccc ngnatgaag cctcncntct ccggcnc 818

<210> 28  
 <211> 731  
 <212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 28

aggaagggcg	gagggatatt	gtangggatt	gagggatagg	agnataangg	gggaggtgtg	60
tcccaacatg	anggtgnngt	tctcttttga	angaggggtg	ngtttttann	ccnggtgggt	120
gattnaaccc	cattgtatgg	agnnaaaggn	tttnagggat	ttttcggtc	ttatcagtat	180
ntanattcct	gtnaatcgga	aaatnatntt	tcnncnggaa	aatnttgctc	ccatccgnaa	240
attnctcccg	ggtagtgcac	nttngggggn	cngccangtt	tcccaggctg	ctanaatcgt	300
actaaagntt	naagtgggan	tncaaagaa	aacctnncac	agagnatccn	taccgcactg	360
tnnnttncct	tcgcctntg	actctgcng	agcccaatac	ccnngngnat	gtcncncngn	420
nnngcgcnc	tgaaannnc	tcnggctnn	gancatcang	gggtttcgca	tcaaaagcnn	480
cgtttcncat	naaggcaact	tngectcatc	caaccnctng	ccctcnncca	tttngccgtc	540
nggttcnctt	acgctnnntg	cncctnnntn	ganattttnc	ccgcctnggg	naancctcct	600
gnaatgggta	gggncttntc	tttnaccnn	gnggtntact	aatcnnctnc	acgcntnctt	660
tctcnacccc	cccccttttt	caatcccanc	ggcnaatggg	gtctccccnn	cgangggggg	720
nnnccannnc	c					731

<210> 29

<211> 822

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(822)

<223> n = A,T,C or G

<400> 29

actagtccag	tgtggtggaa	ttccattgtg	ttggggncnc	ttctatgant	antnttagat	60
cgctcanacc	tcacancctc	ccnacnangc	ctataangaa	nannaataga	nctgtncnnt	120
atntntacnc	tcatanncct	cnnnaccac	tccctcttaa	ccctactgt	gcctatngcn	180
tnnctantct	ntgccgcctn	cnanccaccn	gtgggcnac	cncnngnat	ctcnatctcc	240
tcnccatntn	gcctananta	ngtncatacc	ctataacctac	nccaatgcta	nnnctaancn	300
tccatnantt	annntaacta	ccactgaent	ngactttcnc	atnanctcct	aatttgaatc	360
tactctgact	cccacngcct	annnattagc	ancntcccc	nacnatntct	caaccaaate	420
ntcaacaacc	tatctanctg	ttcnccaacc	nttncctccg	atccccnnac	aaccccccctc	480
ccaaataacc	nccacctgac	ncctaaccn	caccatcccg	gcaagccnan	ggncatttan	540
ccactggaat	cacnatngga	naaaaaaac	ccnaactctc	tancncnnat	ctccctaana	600
aatnctcctn	naatttactn	ncantnccat	caancccaac	tgaaacnnaa	ccccgttttt	660
tanatccctt	ctttcgaaaa	ccnacccttt	annncccaac	ctttngggcc	ccccnctnc	720
ccnaatgaag	gncncccaat	cnangaaacg	nccntgaaaa	ancnaggcna	anannntccg	780
canatcctat	cccttanttn	ggggnccctt	nccnggggcc	cc		822

<210> 30

<211> 787

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature



&lt;222&gt; (1)...(787)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 30

cgccgcctg	ctctggcaca	tgcctcctga	atggcatcaa	aagtgatgga	ctgcccattg	60
ctagagaaga	ccttctctcc	tactgtcatt	atggagccct	gcagactgag	ggctcccctt	120
gtctgcagga	tttgatgtct	gaagtcgtgg	agtgtggctt	ggagctcctc	atctacatna	180
gctggaagcc	ctggagggcc	tctctcgcca	gcctccccct	tctctccacg	ctctccangg	240
acaccagggg	ctccaggcag	cccattattc	ccagnangac	atggtgtttc	tccacgcgga	300
cccatggggc	ctgnaaggcc	aggggtctct	ttgacaccat	ctctcccgtc	ctgcctggca	360
ggcctgggga	tccactantt	ctanaacggg	cgccaccncg	gtgggagctc	cagcttttgt	420
tcccnttaat	gaaggttaat	tgcncgcttg	gcgtaatcat	nggtcanaac	tntttcctgt	480
gtgaaattgt	ttntcccctc	ncnattccnc	ncnacatacn	aacccggaan	cataaagtgt	540
taaagcctgg	gggtngcctn	nngaataaac	tnaactcaat	taattgcgtt	ggctcatggc	600
ccgctttccn	ttcnggaaaa	ctgtcntccc	ctgcnttntt	gaatcggcc	ccccccnggg	660
aaaagcggtt	tgcnttttng	ggggntcctt	ccncttcccc	cctcnctaan	ccctncgect	720
cggtcgttnc	nggtngcggg	gaangggnat	nnnctccnc	naaggggng	agnnngntat	780
ccccaaa						787

&lt;210&gt; 31

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(799)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 31

tttttttttt	tttttttggc	gatgctactg	tttaattgca	ggaggtgggg	gtgtgtgtac	60
catgtaccag	ggctattaga	agcaagaagg	aaggagggag	ggcagagcgc	cctgctgagc	120
aacaaaggac	tctctgcagc	ttctctgtct	gtctcttggc	gcaggcacat	ggggaggcct	180
cccgagggtt	ggggggccacc	agtccagggg	tgggagcact	acanggggtg	ggagtgggtg	240
gtggctggtn	cnaatggcct	gncacanatc	cctacgatct	ttgacacctg	gatttcacca	300
ggggaccttc	tgttctccca	nggnaacttc	ntnnatctcn	aaagaacaca	actgtttctt	360
cngcanttct	ggctgttcat	ggaaagcaca	ggtgtccnat	ttnggctggg	acttggtaca	420
tatggttccg	gcccacctct	cccntcnaan	aagtaattca	cccccccccn	ccntctnttg	480
cctggggcct	taantaccca	caccggaact	canttantta	tctatcttng	gntgggcttg	540
ntnatchccn	cctgaangcg	ccaagttgaa	aggccacgcc	gtncnctc	cccatagnan	600
nttttntnt	canctaatgc	ccccccnggc	aacnatccaa	tcccccccn	tgggggcccc	660
agcccanggc	ccccgnctcg	ggnnccnngn	cncgnantcc	ccaggncttc	ccantcngnc	720
ccnnngcncc	cccgcacgca	gaacanaagg	ntngagccnc	cgcannnnnn	nggtnnncac	780
ctcgcccccc	ccnncgnng					799

&lt;210&gt; 32

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(789)

&lt;223&gt; n = A,T,C or G

```

<400> 32
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt      60
ttttnccnag ggcaggttta ttgacaacct cncgggacac aancaggctg gggacaggac      120
ggcaacaggc tccggcgggcg gcggcgggcg ccctacctgc ggtaccaa atgtcagcctc      180
cgctcccgct tgatnttcct ctgcagctgc aggatgcctt aaaacagggc ctcggcctnt      240
ggtgggcacc ctgggatttn aatttccacg ggcacaatgc ggtcgcancc cctcaccacc      300
nattagggaat agtggtnnta cccnccnccg ttggcncact ccccttgga accacttntc      360
gcggctccgg catctggtct taaaccttgc aaacnctggg gccctctttt tggttantnt      420
nccngccaca atcatnactc agactggcnc gggctggccc caaaaaancn ccccaaaacc      480
ggnccatgtc ttncgggggt tgetgcnatn tncatcacct cccgggcnca ncaggncaac      540
ccaaaagtgc ttgngggccn caaaaaanct ccggggggnc ccagtttcaa caaagtcac      600
ccccttgggc cccaaatcct cccccgntt nctgggtttg ggaacccacg cctctnnctt      660
tggngggcaa gntggntccc ccttcggggc cccgggtggc ccnctctaa ngaaaaacnc      720
ntcctnnnca ccatecccc nngnnacgnc tancaangna tccctttttt tanaaacggg      780
ccccccnccg                                     789

```

<210> 33

<211> 793

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(793)

<223> n = A,T,C or G

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<400> 33
gacagaacat gttggatggt ggagcacctt tctatacgac ttacaggaca gcagatgggg      60
aattcatggc tggttgagca atanaacccc agttctacga gctgctgac aaaggacttg      120
gactaaagtc tgatgaactt cccaatcaga tgagcatgga tgattggcca gaaatgaana      180
agaagtttgc agatgtattt gcaaagaaga cgaaggcaga gtggtgtcaa atctttgacg      240
gcacagatgc ctgtgtgact ccggttctga cttttgagga ggttggtcat catgatcaca      300
acaangaacg gggctcgttt atcaccantg aggagcagga cgtgagcccc cgccctgcac      360
ctctgctgtt aaacacccca gccatccctt ctttcaaaag ggatccacta cttctagagc      420
ggncgccacc gcggtggagc tccagctttt gttcccttta gtgaggggta attgcgcgct      480
tggcgtaatc atggtcatan ctgtttcctg tgtgaaattg ttatccgctc acaattccac      540
acaacatacg anccggaagc atnaaatttt aaagcctggg ggtngcctaa tgantgaact      600
nactcacatt aattggcttt gcgctcactg cccgctttcc agtccggaaa acctgtcctt      660
gccagctgcc nttaatgaat cnggccaccc cccggggaaa aggcngtttg cttnttgggg      720
cgcncttccc gctttctcgc ttcttgaant ccttcccccc ggtctttcgg cttgcggcna      780
acggtatcna cct                                     793

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<210> 34

<211> 756

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(756)

<223> n = A,T,C or G

```

<400> 34
gccgcgaccg gcatgtacga gcaactcaag ggcgagtggg accgtaaaag ccccaatctt      60
ancaagtgcg gggaanagct gggctcgactc aagctagttc ttctggagct caacttcttg      120

```

ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccgtag	catactggag	180
atcggggccc	aatggagcat	cctacgcaan	gacatcccc	ccttcgagcg	ctacatggcc	240
cagctcaa	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttccctg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtccttga	gcaatactga	tggangggcag	ctaccncaa	gtnttcctgg	ccnagggtaa	480
catccccgc	cgagagctac	accttcttca	ttgacatcc	gctcgacact	atcagggatg	540
aaaatcgcn	ggttgtctca	gaaaggctnc	aanaanatcc	tttctnctga	aggcccccg	600
atnctnctagt	nctagaatcg	gccccccatc	gcggtgganc	ctccaacctt	tcgttnccct	660
ttactgaggg	tttattgccc	cccttggcgt	tatcatggtc	acnccngttn	cctgtgttga	720
aattnttaac	cccccaaat	tccacgccna	cattn			756

&lt;210&gt; 35

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (834)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 35

ggggatctct	anactnacct	gnatgcatgg	ttgtcggtgt	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggtc	gctgtnttta	agttgctcag	tctgccgtca	120
tagtcagaca	cnetcttggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcnng	gctgtctgct	cgggtgaactc	gatgaacnang	ggcagctggg	tgtgtntgat	240
aaantccanc	angttctcct	tgggtgacctc	cccttcaaag	ttgttccggc	cttcatcaaa	300
cttctnnaan	angannancc	cantcttgtc	gagctggnat	ttgganaaca	cgtcaccgtt	360
ggaaactgat	cccaaattgg	atgtcatcca	tcgcctctgc	tgccctgcaa	aaacttgctt	420
ggcncaaate	cgactcccn	tccttgaaag	aagccnatca	cacccccctc	cctggactcc	480
nncaangact	ctnccgctnc	cccntccnng	cagggttggg	ggcannccgg	gcccntgcgc	540
ttcttcagcc	agttcacnat	nttcacagc	ccctctgcc	gctgtntat	tccttggggg	600
ggaanccgtc	tctcccttcc	tgaannaact	ttgaccgtng	gaatagccgc	gcntcnccnt	660
acntnctggg	ccgggttcaa	antccctccn	ttgncnntcn	cctcgggcca	ttctggattt	720
nccnaacttt	ttcttccccc	cncctccnng	ngtttgntt	ttcatnggg	ccccactct	780
gctnttggcc	antcccttgg	gggcntntan	cncctccnt	ggcc		834

&lt;210&gt; 36

&lt;211&gt; 814

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (814)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 36

cggncgcttt	ccngccgcgc	cccgtttcca	tgacnaaggc	tcccttcang	ttaaatacnn	60
cctagnaac	attaatgggt	tgctctacta	atacatcata	cnaaccagta	agcctgccca	120
naacgccaac	tcaggccatt	cctaccaaag	gaagaaaggc	tggtctctcc	acccccgtga	180
ggaaaggcct	gccttgtaag	acaccacaat	ncggctgaat	ctnaagtctt	gtgttttact	240
aatggaaaaa	aaaaataaac	aanaggtttt	gttctcatgg	ctgccaccg	cagcctggca	300
ctaaaacanc	ccagcgctca	cttctgcttg	ganaaatatt	ctttgctctt	ttggacatca	360

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ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc 420
antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc 480
aggggagntc ntttncagtg gatctgccaa anantaccn tatcatcnnt gaataaaaag 540
gccccgaac ganatgcttc cancancctt taagacccat aatcctngaa ccatgggtgcc 600
cttccgggtc gatccnaaag gaatgttctt gggctccant cctcctttg ttntttacgt 660
tgtnttggac ccntgctngn atnaccnaan tganatcccc ngaagcacc tnccttggc 720
atgtgantt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcncnaa 780
ggngaactca agaagggtctn ngaaaaacca cncn 814

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&lt;210&gt; 37

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(760)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 37

```

gcatgctgct cttcctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg 60
gcgcagtggt cgctgaaggg gttgtagtac cagcgcgagg tgctctcctt gcagagtcct 120
gtgtctggca ggtccacgca atgccctttg tctactggga aatggatgag ctggagctcg 180
tcnaanccac tcgtgtatctt ttacangca gcctcctccg aagcctccgg gcagttgggg 240
gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt 300
gggctgacag gtgccagaac aactggatn ggcttttcca tggaaagggc tgggggaaat 360
cncctnancc caaactgcct ctcaaaggcc accttgaca ccccgacagg ctgaaatgc 420
actcttcttc ccaaaggtag ttgttcttgt tgcccaagca ncctccanca aaccaaanc 480
ttgcaaaatc tgctccgtgg gggatcnnn taccanggtt ggggaaanaa acccggcngn 540
ganccnctt gtttgaatgc naaggnaata atcctcctgt cttgcttggg tggaanagca 600
caattgaact gttaacnttg ggccnggttc cncnnggtg gtctgaaact aatcacgctc 660
actggaaaaa ggtangtgcc ttccttgaat tcccaaantt cccctngntt tgggtntttt 720
ctcctctncc ctaaaaatcg tnttcccccc ccntangggc 760

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&lt;210&gt; 38

&lt;211&gt; 724

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(724)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 38

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tttttttttt tttttttttt tttttttttt ttttttaaaa cccctccat tgaatgaaaa 60
cttcnaaat tgtccaaccc cctcnccaa atnccattt cggggggggg gttccaaacc 120
caaattaatt ttgganttta aattaaant tnatnngggg aanaanccaa atgtnaagaa 180
aatttaaccc attatnaact taaatnccn gaaacccntg gnttccaaaa atttttaacc 240
cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaagggt 300
ngatttaaac ccccttnant tnttttnacc cngnctnaa ntatttngnt tccggtgttt 360
tcctntaan cntnggtaac tcccngtaac gaannnccct aanccaatta aaccgaattt 420
tttttgaatt ggaattccn ngggaattna cgggggtttt tccnttttg gggccatncc 480
ccnctttcg ggggttgggn ntaggttgaa tttttnnang ncccaaaaaa nccccaana 540
aaaaaactcc caagnnttaa ttngaanttc ccccttccca ggctttttgg gaaagnggg 600

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ttnttggggg ccngggantt cnttccccn ttncncccc cccccnggt aaanggttat	660
ngnntttggt ttttgggccc cttnanggac cttccggatn gaaattaaat ccccggnncg	720
gccg	724

&lt;210&gt; 39

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(751)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 39

tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca	60
caacacaata tttatttcat ttgtttcttt tattttcattt tatttggttg ctgctgctgt	120
tttatttatt ttactgaaa gtgagaggga acttttgttg ctttttttcc tttttctgta	180
ggccgcctta agctttctaa atttggaaac tctaagcaag ctgaanggaa aagggggttt	240
cgcaaatca ctcgggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga	300
ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaangc ttttaattana	360
cttgggggtt ccttccccc accaaccnccn ctgacaaaaa gtgccngccc tcaaatnatg	420
tcccgcnnt cnttgaaaca cacngcngaa ngttctcatt ntcccccnc caggtnaaaa	480
tgaagggtta ccatntttaa cncacctcc acntggcnnn gcctgaatcc tcnaaaancn	540
cctcaancn aattnctnng ccccggtcnc gcntnngtcc cncgcgggt cggggaantn	600
cacccccnga annnntnnc naacnaaatt ccgaaaatat tcccnntcnc tcaattcccc	660
cnnagactnt cctcnnncn cncaattttc tttntntcac gaacncgnnc cnnaaaatgn	720
nnnnncctc cncnngtcn naatcnccan c	751

&lt;210&gt; 40

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(753)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 40

gtggtatttt ctgtaagatc aggtgttcct ccctcgtagg tttagaggaa acaccctcat	60
agatgaaaac ccccccgaga cagcagcact gcaactgcca agcagccggg gtaggagggg	120
cgccctatgc acagctgggc ccttgagaca gcagggttc gatgtcaggc tcgatgtcaa	180
tgggtctggaa gcggcggctg tacctgcgta ggggcacacc gtcaggggcc accaggaact	240
tctcaaagt ccaggcaacn tcgttgcgac acaccggaga ccagggtgatn agcttggggt	300
cggtcataa cgcgggtggc tcgtcgctgg gagctggcag ggcctccgc aggaaggcna	360
ataaaagggt cgccccgca cgttcantc cgcacttctc naanaccatg angttgggct	420
cnaaccacc accannccg acttccttga nggaattccc aaatctcttc gntcttgggc	480
ttctnctgat gccctanctg gttgcccn gncccaancc cgggggtcct	540
aaanaccn cctctcntt tcactctgggt tntntcccc ggaccttggg tctctcaag	600
ggancccata tctcnaccn tactcacnt nccccccnt gnnaccanc cttctanngn	660
tcccccccg nctctggcc cntcaaan gcttnacna cctgggtctg cttcccccc	720
tncctatct gnacccn tttgtctcan tnt	753

&lt;210&gt; 41

<211> 341  
 <212> DNA  
 <213> Homo sapien

<400> 41  
 actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaagt 60  
 agtgaaccca tccttgattt atatacatat atgttctcag tattttggga gcctttccac 120  
 ttctttaaac cttgttcatt atgaacactg aaaataggaa tttgtgaaga gtaaaaagt 180  
 tatagcttgt ttacgtagta agtttttgaa gtctacattc aatccagaca cttagttgag 240  
 tgttaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat 300  
 ttttactttt tgattaattg tgttttatat attagggtag t 341

<210> 42  
 <211> 101  
 <212> DNA  
 <213> Homo sapien

<400> 42  
 acttactgaa tttagtcttg tgctcttcct tatttagtgt tgtatcataa atactttgat 60  
 gtttcaaaca ttctaaataa ataattttca gtggcttcat a 101

<210> 43  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 43  
 acatctttgt tacagtctaa gatgtgttct taaatcacca ttcttctctg gtcctcaccc 60  
 tccaggtggt tctcacactg taatttagagc tattgaggag tctttacagc aaattaagat 120  
 tcagatgcct tgctaagtct agagttctag agttatgttt cagaaagtct aagaaacca 180  
 cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat 240  
 tggatacaga acgagagtta tcctggataa ctacagagctg agtacctgcc cgggggcccgc 300  
 tcgaa 305

<210> 44  
 <211> 852  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(852)  
 <223> n = A,T,C or G

<400> 44  
 acataaatat cagagaaaag tagtctttga aatatttacg tccaggagtt ctttgtttct 60  
 gattatttgg tgtgtgtttt ggtttgtgtc caaagtattg gcagcttcag ttttcatttt 120  
 ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct 180  
 ccagaatttc tcttttgtag taatatctca tagctcggct gagcttttca taggtcatgc 240  
 tgctgttgtt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga 300  
 agacgccctc agatcggtct tcccatttta ttaatcctgg gttcttgtct gggttcaaga 360  
 ggatgtcgcg gatgaattcc cataagttag tccctctcgg gttgtgcttt ttgggtgagg 420  
 acttggcagg ggggtccttg tcctttttca tatcaggtga ctctgcaaca ggaaggtgac 480  
 tggtgggtgt catggagatc tgagcccggc agaaagtttt gctgtccaac aaatctactg 540  
 tgctaccata gttggtgtca tataaatagt tctngtcttt ccagggtgtc atgatggaag 600

gctcagtttg	ttcagtcttg	acaatgacat	tgtgtgtgga	ctggaacagg	tcactactgc	660
actggccggt	ccacttcaga	tgetgcaagt	tgctgtagag	gagntgcccc	gccgtccctg	720
ccgcccgggt	gaactcctgc	aaactcatgc	tgcaaagggt	ctcgccggtg	atgtcgaact	780
cntggaaagg	gatacaattg	gcatccagct	ggttggtgtc	caggagggtga	tggagccact	840
cccacacctg	gt					852

&lt;210&gt; 45

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 45

acaacagacc	cttgctcgct	aacgacctca	tgctcatcaa	gttggaacgaa	tcctgtgccg	60
agtctgacac	catccggagc	atcagcattg	cttcgcagtg	ccctaccgcg	gggaactcct	120
gcctcgtttc	tggctgggggt	ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	180
tgaacgtgtc	ggtggtgtct	gaggaggtct	gcagtaagct	ctatgaccgg	ctgt	234

&lt;210&gt; 46

&lt;211&gt; 590

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (590)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 46

actttttatt	taaatgttta	taaggcagat	ctatgagaat	gatagaaaac	atggtgtgta	60
atttgatagc	aatatttttg	agattacaga	gttttagtaa	ttaccaatta	cacagttaaa	120
aagaagataa	tatattccaa	gcanatacaa	aatatcta	gaaagatcaa	ggcaggaaaa	180
tgantataac	taattgacaa	tggaaaatca	attttaatgt	gaattgcaca	ttatccttta	240
aaagctttca	aaanaanaa	ttattgcagt	ctanttaatt	caaacagtgt	taaatggtat	300
caggataaan	aactgaaggg	canaaagaat	taattttcac	ttcatgtaac	ncacccanat	360
ttacaatggc	ttaaatgcan	ggaaaaagca	gtggaagtag	ggaagtantc	aaggctcttc	420
tggctcttaa	tctgccttac	tctttgggtg	tggctttgat	cctctggaga	cagctgccag	480
ggctcctggt	atatccacaa	tcccagcagc	aagatgaagg	gatgaaaaag	gacacatgct	540
gccttccttt	gaggagactt	catctcactg	gccaacactc	agtcacatgt		590

&lt;210&gt; 47

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (774)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 47

acaagggggc	ataatgaagg	agtggggana	gattttaaag	aaggaaaaaa	aacgaggccc	60
tgaacagaat	tttctgnac	aacggggctt	caaaataatt	ttcttgggga	ggttcaagac	120
gcttctactgc	ttgaaactta	aatggatgtg	ggacanaatt	ttctgtaatg	accctgaggg	180
cattacagac	gggactctgg	gaggaaggat	aaacagaaag	gggacaaaag	ctaattcccaa	240
aacatcaaag	aaaggaaggt	ggcgtcatac	ctcccagcct	acacagttct	ccagggctct	300

```

cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtg 360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgctgat cctgcgtggc 420
ccacactcct tgaacacaca tccccaggtt atattcctgg acatggctga acctcctatt 480
cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc 540
acggcatggg aagcctttct gacttgctg attactccag catcttgga caatccctga 600
ttccccactc cttagaggca agatagggg gttaagagta gggctggacc acttgagacc 660
aggetgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct 720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt 774

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&lt;210&gt; 48

&lt;211&gt; 124

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(124)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 48

```

canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt 60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact 120
tggt 124

```

&lt;210&gt; 49

&lt;211&gt; 147

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(147)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 49

```

gccgatgcta ctattttatt gcaggaggtg ggggtgtttt tattattctc tcaacagctt 60
tgtggctaca ggtgggtgtc gactgcatna aaaantttt tacgggtgat tgcaaaaatt 120
ttagggcacc catatcccaa gcantgt 147

```

&lt;210&gt; 50

&lt;211&gt; 107

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 50

```

acattaaatt aataaaagga ctgttggggg tctgctaaaa cacatggctt gatatatgtc 60
atggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

```

&lt;210&gt; 51

&lt;211&gt; 204

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 51

```

gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgcacgg 60

```



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cggaaggaa aggcagagaa gtgacaccgt caggggggaaa tgacagaaag gaaaatcaag    120
gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttggcca    180
cctccctttt gggaccagca atgt                                           204

```

&lt;210&gt; 52

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(491)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 52

```

acaaagataa catattatctt ataacaaaaa tttgatagtt ttaaagggtta gtattgtgta    60
gggtattttt caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca    120
ccatcagaca ggttttttaa aaacaacata ttacaaaatt agacaatcat ctttaaaaaa    180
aaaactttct gtatcaattt cttttgttca aaatgactga cttaantatt tttaaatatt    240
tcanaaacac ttcctcaaaa attttcaana tggtagcttt canatgtnc ctcagtccca    300
atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc    360
atgcaacagt gtcttttctt tnccttttct tttttttttt ttacaggcac agaaactcat    420
caattttatt tggataacaa aggtgtctcca aatttatattg aaaaataaat ccaagttaat    480
atcactcttg t                                           491

```

&lt;210&gt; 53

&lt;211&gt; 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(484)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 53

```

acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga    60
gtattaacag ttgctgaagt ttggtatttt tatgcagcat tttctttttg ctttgataac    120
actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct    180
caatcaaadc tctacataac actatagtaa ttaaaacggt aaaaaaaagt gttgaaatct    240
gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc    300
agctttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttggt gcctctccct    360
aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg    420
tancttgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc    480
cant                                           484

```

&lt;210&gt; 54

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 54

```

actaaacctc gtgcttgatg actccataca gaaaacgggt ccattccctga acacggctgg    60
ccactgggta tactgctgac aaccgcaaca caaaaaacac aaatccttgg cactggctag    120
tctatgtcct ctcaagtgcc tttttgtttg t                                           151

```

<210> 55  
 <211> 91  
 <212> DNA  
 <213> Homo sapien

<400> 55  
 acctggcttg tctccgggtg gttcccggcg cccccacgg tccccagaac ggacactttc 60  
 gccctccagt ggatactcga gccaaagtgg t 91

<210> 56  
 <211> 133  
 <212> DNA  
 <213> Homo sapien

<400> 56  
 ggcggatgtg cgttggttat atacaaatat gtcattttat gtaagggact tgagtatact 60  
 tggatttttg gtatctgtgg gttgggggga cgggccagga accaataccc catggatacc 120  
 aagggaacaac tgt 133

<210> 57  
 <211> 147  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (147)  
 <223> n = A,T,C or G

<400> 57  
 actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60  
 gactgggagc tgagcccttc cctttgcgcc tgccctcagag gattgttgcc gacntgcana 120  
 tctcantggg ctggatncat gcagggt 147

<210> 58  
 <211> 198  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (198)  
 <223> n = A,T,C or G

<400> 58  
 acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60  
 tgattacata catttatcct ttaaaaaaga tgtaaatctt aatttttatg ccatctatta 120  
 atttaccat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180  
 ttgacttcta agtttggt 198

<210> 59  
 <211> 330  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 59

acaacaaatg ggttgtagg aagtcttata agcaaaactg gtgatggcta ctgaaaagat	60
ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt	120
cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa	180
tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagaccag	240
cagaaggaaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt	300
tttcgtcttt attggacttc tttgaagagt	330

&lt;210&gt; 60

&lt;211&gt; 175

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 60

accgtgggtg ccttctacat tcctgacggc tccttcacca acatctgggt ctacttcggc	60
gtcgtgggct ccttctctct catcctcctc cagctgggtg tgctcatcga ctttgcgac	120
tcctggaacc agcgggtggc gggcaaggcc gaggagtgcg attcccgtgc ctgggt	175

&lt;210&gt; 61

&lt;211&gt; 154

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 61

acccacttt tcctcctgtg agcagtctgg acttctcact gctacatgat gaggtgag	60
ggttggtgct cttcaacagt atcctcccct ttccggatct gctgagccgg acagcagtgc	120
tggactgcac agccccggg ctccacattg ctgt	154

&lt;210&gt; 62

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 62

cgctcgagcc ctatagttag tcgtattaga	30
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&lt;210&gt; 63

&lt;211&gt; 89

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 63

acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc	60
ctgtatgaat aaaaatggtt atgtcaagt	89

&lt;210&gt; 64

&lt;211&gt; 97

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 64

accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag	60
aatcagtgc tccaggattg gtccttggat ctgggg	97

<210> 65  
 <211> 377  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(377)  
 <223> n = A,T,C or G

<400> 65  
 acaacaanaa ntcccttctt taggccactg atggaaacct ggaaccccct tttgatggca 60  
 gcatggcgct ctaggccttg acacagcggc tgggggttgg gctntcccaa accgcacacc 120  
 ccaaccctgg tctaccacaca nttctggcta tgggctgtct ctgccactga acatcagggg 180  
 tcggtcataa natgaaatcc caanggggac agaggtcagt agagggaagct caatgagaaa 240  
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300  
 tgggggtgaa ctaccccccag gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360  
 gggcggggagg agcatgt 377

<210> 66  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 66  
 acgcctttcc ctcagaattc agggaagaga ctgtcgctg ccttcctccg ttgttgctg 60  
 agaaccctg tgccccctcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120  
 aggaactaac tgcaccctgg tcctctcccc agtccccagt tcaccctcca tccctcacct 180  
 tcctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt 240  
 ttatatattt tttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300  
 tgttt 305

<210> 67  
 <211> 385  
 <212> DNA  
 <213> Homo sapien

<400> 67  
 actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60  
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcaggt ctgagagttc 120  
 cccttttaaa aaaggggact tgcttaaaaa agaagcttag ccacgattgt gtagagcagc 180  
 tgtgctgtgc tggagattca cttttgagag agttctcctc tgagacctga tctttagagg 240  
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300  
 cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac 360  
 catagtttct gtgctagtgg accgt 385

<210> 68  
 <211> 73  
 <212> DNA  
 <213> Homo sapien

<400> 68  
 acttaaccag atatatatttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60  
 gtttttttaa tgg 73

<210> 69  
 <211> 536  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(536)  
 <223> n = A,T,C or G

<400> 69  
 actagtccag tgtggtggaa ttccattgtg ttggggggctc tcaccctcct ctccctgcagc 60  
 tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120  
 cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180  
 cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240  
 cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggt 300  
 actaagagcc aggaacaga ccgttggggg ggtgaattac ttcttcgacg tagaggtggg 360  
 ccgaaccata tgtaccaagt ccagcccaa cttggacacc tgtgccttcc atgaacagcc 420  
 agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagttccct ggggagaaca 480  
 gaangtcctt ggggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70  
 <211> 477  
 <212> DNA  
 <213> Homo sapien  
 <400> 70

atgaccctta acagggggccc tctcagccct cctaattgacc tccggcctag ccatgtgatt 60  
 tcacttccac tccataacgc tcctcatact aggcctacta accaacacac taaccatata 120  
 ccaatgatgg cgcgatgtaa cacgagaaag cacataccaa ggccaccaca caccacctgt 180  
 ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc 240  
 agggattttt ctgagccttt taccactcca gcctagcccc tacccccacaa ctaggagggc 300  
 actggccccc aacaggcatc accccgctaa atcccctaga agtcccactc ctaaacacat 360  
 ccgtattact cgcattcagga gtatcaatca cctgagctca ccatagtcta atagaaaaca 420  
 accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatttt 477

<210> 71  
 <211> 533  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(533)  
 <223> n = A,T,C or G

<400> 71  
 agagctatag gtacagtgtg atctcagctt tgcaaàcaca ttttctacat agatagtact 60  
 aggtattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattgggtta 120  
 tgtgatttta gtggattttt tggcaccctt atatatgttt tccaaacttt cagcagtgat 180  
 attatttcca taacttaaaa agtgagtgtt aaaaagaaaa tctccagcaa gcatctcatt 240  
 taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagtgtgc 300  
 aaatagggtg gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360  
 agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420  
 cttcgttaatt ttggagtang aggttccctc ctcaattttg tattttttaa aagtacatgg 480  
 taaaaaaaaa aattcacacac agtatataag gctgtaaaaat gaagaattct gcc 533

<210> 72  
 <211> 511  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(511)  
 <223> n = A,T,C or G

<400> 72  
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta 60  
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120  
 aagccgcagg atgtctacac tatancaggc gctatattggg ttggctggag gagctgtgga 180  
 aaacatggan agattggtgc tgganatcgc cgtggctatt cctcattgtt attacanagt 240  
 gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300  
 cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac 360  
 gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg 420  
 atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggt atgatggcna 480  
 aaatacaccc cctcttgaag naccnggagg a 511

<210> 73  
 <211> 499  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(499)  
 <223> n = A,T,C or G

<400> 73  
 cagtgccagc actggtgcca gtaccagtac caataacagt gccagtgccca gtgccagcac 60  
 cagtgggtggc ttcagtgtg gtgccagcct gaccgccact ctcacatttg ggctcttcgc 120  
 tggccttggt ggagctggtg ccagcaccag tggcagctct ggtgcctgtg gtttctccta 180  
 caagtgagat tttagatatt gttaatcctg ccagtctttc tcttcaagcc aggggtgcac 240  
 ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca 300  
 ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaaggg cggccgctcg 360  
 antctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420  
 catctgttgt ttgccctcc cccgntgcct tccttgacc tggaaagtgc cactccact 480  
 gtcctttcct aantaaat 499

<210> 74  
 <211> 537  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(537)  
 <223> n = A,T,C or G

<400> 74  
 tttcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gcgaagagat 60

ttatcagctt	aactcagata	aatcattga	aagtaataag	gtaaaagcta	gtctctaact	120
tccaggccca	cggctcaagt	gaatttgaat	actgcattta	cagtgtagag	taacacataa	180
cattgtatgc	atggaaacat	ggaggaacag	tattacagt	tcctaccact	ctaatacaaga	240
aaagaattac	agactctgat	tctacagtga	tgattgaatt	ctaaaaatgg	taatcattag	300
ggcttttgat	ttataaanact	ttgggtactt	atactaaatt	atggtagtta	tactgccttc	360
cagtttgctt	gatataattg	ttgatattaa	gattccttgac	ttatatattt	aatgggttct	420
actgaaaaan	gaatgatata	ttcttgaaga	catcgatata	catttattta	cactcttgat	480
tctacaatgt	agaaaatgaa	ggaaatgccc	caaattgtat	ggtgataaaa	gtcccgct	537

&lt;210&gt; 75

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(467)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 75

caaanacaat	tggtcaaaag	atgcaaatga	tacactactg	ctgcagctca	caaacacctc	60
tgcatattac	acgtacctcc	tcctgtctct	caagtagtgt	ggtctatatt	gccatcatca	120
cctgtgtgt	gcttagaaga	acggctttct	gctgcaangg	agagaaatca	taacagacgg	180
tggcacaagg	aggccatctt	ttcctcatcg	gttattgtcc	ctagaagcgt	cttctgagga	240
tctagttggg	ctttctttct	gggtttgggc	catttcantt	ctcatgtgtg	tactattcta	300
tcattattgt	ataacgggtt	tcaaaccngt	gggcacncag	agaacctcac	tctgtaataa	360
caatgaggaa	tagccacggg	gatctccagc	accaaattct	tccatgttnt	tccagagctc	420
ctccagccaa	cccaaatagc	cgctgctatn	gtgtagaaca	tccttgn		467

&lt;210&gt; 76

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(400)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 76

aagctgacag	cattcggggc	gagatgtctc	gctccgtggc	cttagctgtg	ctcgcgctac	60
tctctctttc	tggcctggag	gctatccagc	gtactccaaa	gattcaggtt	tactcacgtc	120
atccagcaga	gaatggaaag	tcaaatttcc	tgaattgcta	tgtgtctggg	tttcatccat	180
ccgacattga	agttgactta	ctgaagaatg	gagagagaat	tgaaaaagtg	gagcattcag	240
acttgtcttt	cagcaaggac	tggtctttct	atctcttgta	ctacactgaa	ttcaccacca	300
ctgaaaaaga	tgagtatgcc	tgccgtgtga	accatgtgac	tttgtcacag	cccaagatng	360
ttnagtggga	tcganacatg	taagcagcan	catgggaggt			400

&lt;210&gt; 77

&lt;211&gt; 248

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 77

ctggagtgcc	ttggtgtttc	aagcccctgc	aggaagcaga	atgcaccttc	tgaggcacct	60
------------	------------	------------	------------	------------	------------	----

```

ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgctgc   120
caggcactgt tcatctcagc ttttctgtcc ctttgcctcc ggcaagcgct tctgctgaaa   180
gttcataatc ggagcctgat gtcttaacga ataaagggtcc catgctccac ccgaaaaaaaa   240
aaaaaaaaa                                     248

```

```

<210> 78
<211> 201
<212> DNA
<213> Homo sapien

```

```

<400> 78
actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca   60
tcacccagac ccgcccctgc ccgtgcccac cgctgctgct aacgacagta tgatgcttac   120
tctgctactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataaatgcct   180
gatttaaaaa aaaaaaaaaa a                                     201

```

```

<210> 79
<211> 552
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (552)
<223> n = A,T,C or G

```

```

<400> 79
tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg   60
tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt   120
cctctttctt ctgaagatta atgaagtga aaattgaggt ggataaatac aaaaaggtag   180
tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt   240
atgcaagtta gtaattactc aggggttaact aaattacttt aatatgctgt tgaacctact   300
ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga   360
taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta   420
ttcccaggaa tatgggggtc atttatgaat antaccggg anagaagttt tgantnaaac   480
cngttttggt taatacgta atatgtcctn aatnaacaag gcntgactta tttccaaaaa   540
aaaaaaaaa aa                                     552

```

```

<210> 80
<211> 476
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (476)
<223> n = A,T,C or G

```

```

<400> 80
acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga   60
ggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct   120
cacacagact ccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt   180
gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta   240
aggttaaact ttcccacca gaaaaggcaa cttagataaa atcttagagt actttcatac   300
tcttctaagt cctcttcag cctcactttg agtcctcctt ggggggttgat aggaantntc   360

```



tcttggcttt	ctcaataaaa	tctctatcca	tctcatgttt	aatttggtac	gcntaaaaat	420
gctgaaaaaa	ttaaaatggt	ctggtttcnc	tttaaaaaaa	aaaaaaaaaa	aaaaaa	476

<210> 81  
 <211> 232  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(232)  
 <223> n = A,T,C or G

<400> 81						
tttttttttg	tatgcctcn	ctgtggngtt	attgttgctg	ccaccctgga	ggagcccagt	60
ttcttctgta	tctttctttt	ctgggggatc	ttcctggctc	tgccctcca	ttcccagcct	120
ctcatcccca	tcttgacttt	ttgctagggt	tggaggcgct	ttcctggtag	cccctcagag	180
actcagtcag	cggaataag	tcctaggggt	ggggggtgtg	gcaagccggc	ct	232

<210> 82  
 <211> 383  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(383)  
 <223> n = A,T,C or G

<400> 82						
aggcgggagc	agaagctaaa	gccaaagccc	aagaagagt	gcagtgccag	cactggtgcc	60
agtaccagta	ccaataacat	gccagtgcc	gtgccagcac	cagtgggtggc	ttcagtgtg	120
gtgccagcct	gaccgccact	ctcacatttg	ggctcttcgc	tggccttggg	ggagctggg	180
ccagcaccag	tggcagctct	ggtgcctgtg	gtttctccta	caagtgagat	tttagatatt	240
gttaatcctg	ccagtctttc	tcttcaagcc	aggggtgcac	ctcagaaacc	tactcaacac	300
agcactctng	gcagccacta	tcaatcaatt	gaagttgaca	ctctgcatta	aatctatttg	360
ccattttcaaa	aaaaaaaaaa	aaa				383

<210> 83  
 <211> 494  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(494)  
 <223> n = A,T,C or G

<400> 83						
accgaattgg	gaccgctggc	ttataagcga	tcatgtcctc	cagtattacc	tcaacgagca	60
gggagatcga	gtctatacgc	tgaagaaatt	tgacccgatg	ggacaacaga	cctgctcagc	120
ccatcctgct	cggttctccc	cagatgacaa	atactctcga	caccgaatca	ccatcaagaa	180
acgcttcaag	gtgctcatga	cccagcaacc	gcgcctgtc	ctctgagggt	ccttaaactg	240
atgtcttttc	tgccacctgt	taccctctcg	agactccgta	accaaactct	tcggactgtg	300
agccctgatg	cctttttgcc	agccatactc	tttggcntcc	agtctctcgt	ggcgattgat	360

```

tatgcttgtg tgaggcaatc atggtggcat cacccatnaa gggaacacat ttganttttt 420
tttcncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta 480
aaaaaaaaaa aaaa 494

```

```

<210> 84
<211> 380
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

```

```

<400> 84
gctggtagcc tatggcgtgg ccacggangg gtcctgagg cacgggacag tgacttccca 60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120
gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttcttg 180
gcacaccctc ctggggccca ggcgggcacc tgcgtctccc agtatgccaa ctggctggtg 240
gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg 300
ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
agcgttnccg cctcatccgg 480

```

```

<210> 85
<211> 481
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

```

```

<400> 85
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc 60
tnccatcgtc atactgtagg tttgccacca ctcctgcat cttggggcgg ctaatatcca 120
ggaaactctc aatcaagtca ccgctcnatna aacctgtggc tggttctgtc ttccgctcgg 180
tgtgaaagga tctccagaag gagtgctcga tcttccccac acttttgatg actttattga 240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtgag gtcaccagcc 300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggg gnagtctcac 360
ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggnngaa 420
aaagaacacc tcctggaagt gctngccgct cctcgctcct tggtggnngc gcntnccttt 480
t 481

```

```

<210> 86
<211> 472
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

```

```

<400> 86

```

```

aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt      60
acttggaaaa gcaacttnaa gcctggacac tggattataa attcacaata tgcaacactt      120
taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg      180
ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct ttttttttga      240
cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcacttttctt      300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg      360
atatntgagc ggaagantag cttttctact tcaccagaca caactccttt catattggga      420
tgtnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg              472

```

&lt;210&gt; 87

&lt;211&gt; 413

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (413)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 87

```

agaaaccagt atctctnaaa acaacctctc ataccttggt gacctaatTT tgtgtgcgtg      60
tgtgtgtgcg cgcatattat atagacaggc acatcttttt tacttttgta aaagcttatg      120
cctcttttgg atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct      180
ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg      300
ggggacaaaag aaaagcnaaa ctgaacatna gaaacaattn cctggtgaga aattncataa      360
acagaaattg ggtngtatat tgaaanang catcattnaa acgttttttt ttt              413

```

&lt;210&gt; 88

&lt;211&gt; 448

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (448)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 88

```

cgcagcgggt cctctctatc tagctccagc ctctcgctg cccactccc cgcgtcccgc      60
gtcctagccn accatggccg ggccccctgc cgccccgctg ctctgctgg ccatcctggc      120
cgtggccctg gccgtgagcc ccgcggcccg ctccagtcce ggcaagccgc cgcgcctggt      180
gggaggccca tggaccccg cgtggaagaag aagggtgtgc gcgtgcactg gactttgccg      240
tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgctgcag gttgtgccgc      300
cccaancaaa ttgttactng gggtaaantaa ttcttggaag ttgaacctgg gccaaacnng      360
tttaccagaa ccnagccaat tngaacaatt nccccccat aacagcccc tttaaaaagg      420
gaancantcc tgntcttttc caaatTTT              448

```

&lt;210&gt; 89

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(463)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 89

gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca	60
gtagtatttc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaatttagc	120
agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt	180
ctcagtgaca agttntttct gatgcgaagt tctnattcca gtgttttagt cctttgcac	240
tttnatgttn agacttgcct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg	300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn	360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn	420
aattcnnana anttcagntn tcatacaaca naacngganc ccc	463

&lt;210&gt; 90

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(400)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 90

agggattgaa ggtctnttnt actgtcggac tgttcancca ccaactctac aagttgctgt	60
cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaaat	120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttccact	180
tcctttgtta agacttcac	240
cgttctctaa caatgtcctc tccttgaagt atttggctga acaaccacc tnaagtcct	300
ttgtgcatcc attttaaata tacttaatag ggcattggtn cactaggtta aattctgcaa	360
gagtcactctg tctgcaaaag ttgcgttagt atatctgcca	400

&lt;210&gt; 91

&lt;211&gt; 480

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(480)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 91

gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact	60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac	120
atgcctcttt gactaccgtg tgccagtgtt ggtgattctc acacacctcc nncgcctctt	180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttaciaaat tcaaccacga	240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt	300
tgtcaatact aaccgcgtgg tttgcctcca tcacatttgt gatctgtagc tctggatata	360
tctctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt	420
ngatcagggt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa	480

&lt;210&gt; 92

&lt;211&gt; 477

&lt;212&gt; DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 92

atacagccca	natccccacca	cgaagatgcg	cttggttgact	gagaacctga	tgcggtcact	60
gggtcccgtg	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgcactcctt	120
cccacgcagg	cagcagcggg	gccggtcaat	gaactccact	cgtggcttgg	ggttgacggt	180
taantgcagg	aagaggctga	ccacctcgcg	gtccaccagg	atgcccgaact	gtgcgggacc	240
tgcagcga	ctcctcgatg	gtcatgagcg	ggaagcgaat	gangcccagg	gccttgccca	300
gaaccttccg	cctgttctct	ggcgtcacct	gcagctgctg	ccgctnacac	tcggcctcgg	360
accagcggac	aaacggcggt	gaacagccgc	acctcacgga	tgcccantgt	gtcgcgctcc	420
aggaacggcn	ccagcgtgtc	caggtcaatg	tcggtgaanc	ctccgcgggt	aatggcg	477

<210> 93

<211> 377

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(377)

<223> n = A,T,C or G

<400> 93

gaacggctgg	acctgcctc	gcattgtgct	gctggcagga	ataccttggc	aagcagctcc	60
agtccgagca	gccccagacc	gctgccgccc	gaagctaagc	ctgcctctgg	ccttccccctc	120
cgcctcaatg	cagaaccant	agtgggagca	ctgtgttttag	agttaagagt	gaacactgtn	180
tgattttact	tgggaatttc	ctctgttata	tagcttttcc	caatgcta	ttccaaacaa	240
caacaacaaa	ataacatgtt	tgctgtttna	gttggtataaa	agtangtgat	tctgtatnta	300
aagaaaatat	tactgttaca	tatactgctt	gcaanttctg	tattttattgg	tnctctggaa	360
ataaatatat	tattaaa					377

<210> 94

<211> 495

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(495)

<223> n = A,T,C or G

<400> 94

ccctttgagg	ggttagggtc	cagttcccag	tgggaagaaac	aggccaggag	aantgcgtgc	60
cgagctgang	cagatttccc	acagtgacc	cagagccctg	ggctatagtc	tctgaccctt	120
ccaaggaaag	accaccttct	ggggacatgg	gctggagggc	aggacctaga	ggcaccaagg	180
gaaggcccca	ttccggggct	gttccccgag	gaggaaggga	aggggctctg	tgtgcccccc	240
acgaggaana	ggccctgant	cctgggatca	nacacccctt	cacgtgtatc	cccacacaaa	300
tgcaagctca	ccaaggtccc	ctctcagtc	cttccctaca	ccctgaacgg	ncactggccc	360
acacccaccc	agancancca	cccgccatgg	ggaatgtnt	caaggaatcg	cngggcaacg	420
tggactctng	tcccnnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480

aaaaaaaaana aaaaa

495

<210> 95  
 <211> 472  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(472)  
 <223> n = A,T,C or G

&lt;400&gt; 95

ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgccgag	agcggacttt	gtaattgttg	gagaataact	gctgaatttt	120
tagctgtttt	gagttgattc	gcaccactgc	accacaactc	aatatgaaaa	ctatttnact	180
tatttattat	cttgtgaaaa	gtatacaatg	aaaattttgt	tcatactgta	tttatcaagt	240
atgatgaaaa	gcaatagata	tatattcttt	tattatgttn	aattatgatt	gccattatta	300
atcggcacaaa	tgtggagtgt	atgttccttt	cacagtaata	tatgcctttt	gtaacttcac	360
ttggttattt	tattgtaa	gaattacaaa	attcttaatt	taagaaaatg	gtangttata	420
tttanttcan	taatttcttt	ccttgtttac	gttaattttg	aaaagaatgc	at	472

<210> 96  
 <211> 476  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(476)  
 <223> n = A,T,C or G

&lt;400&gt; 96

ctgaagcatt	tcttcaaact	tntctacttt	tgtcattgat	acctgtagta	agttgacaat	60
gtggtgaaat	ttcaaaatta	tatgtaactt	ctactagttt	tactttctcc	cccaagtctt	120
ttttaactca	tgatttttac	acacacaatc	cagaacttat	tatatagcct	ctaagtcttt	180
attcttcaca	gtagatgatg	aaagagtcc	ccagtgtcct	gngcanaatg	ttctagntat	240
agctggatac	atacngtggg	agttctataa	actcatacct	cagtgggact	naaccaaaat	300
tgtgttagtc	tcaattccta	ccacactgag	ggagcctccc	aaatcactat	attcttatct	360
gcaggtagtc	ctccagaaaa	acngacaggg	caggcttgca	tgaaaaagtn	acatctgcgt	420
tacaaagtct	atcttcctca	nangtctgtn	aaggaacaat	ttaatcttct	agcttt	476

<210> 97  
 <211> 479  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(479)  
 <223> n = A,T,C or G

&lt;400&gt; 97

actcttttcta	atgctgatat	gatcttgagt	ataagaatgc	atatgtcact	agaatggata	60
aaataatgct	gcaaaacttaa	tgttcttatg	caaaatggaa	cgctaatagaa	acacagctta	120

caatcgcaaa	tcaaaactca	caagtgtctca	tctgtttag	atttagtgta	ataagactta	180
gattgtgtctc	cttcggatat	gattgtttct	canatcttgg	gcaatnttcc	ttagtcaaat	240
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&lt;210&gt; 98

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 98

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&lt;210&gt; 99

&lt;211&gt; 171

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 99

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&lt;210&gt; 100

&lt;211&gt; 269

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 100

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&lt;210&gt; 101

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 101

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<212> DNA

<213> Homo sapien

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<211> 581

<212> DNA

<213> Homo sapien

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<212> DNA

<213> Homo sapien

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<211> 538

<212> DNA



&lt;213&gt; Homo sapien

&lt;400&gt; 105

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&lt;210&gt; 106

&lt;211&gt; 473

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 106

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&lt;210&gt; 107

&lt;211&gt; 1621

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 107

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<213> Homo sapien

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35 40 45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50 55 60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65 70 75 80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85 90 95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
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Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115 120 125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
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Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
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Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
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Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
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Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
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Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
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<211> 3410
<212> DNA
<213> Homo sapien
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tagcgggggtg	aatatttttat	actgtaagtg	agcaatcaga	gtataatgtt	tatgggtgaca	3300
aaattaaagg	ctttctttata	tgtttaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	3360
aaaaaaaaara	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaataa	aaaaaaaaaa		3410

&lt;210&gt; 111

&lt;211&gt; 1289

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 111

```

agccaggcgt ccctctgcct gccactcag tggcaacacc cgggagctgt tttgtccttt      60
gtggagcctc agcagttccc tctttcagaa ctactgcca agagccctga acaggagcca      120
ccatgcagtg cttcagcttc attaaagacca tgatgatcct cttcaatttg ctcactcttc      180
tgtgtggtgc agccctggtg gcagtgggca tctgggtgtc aatcgatggg gcaccccttc      240
tgaagatctt cgggccactg tcgtccagtg ccatgcagtt tgtcaacgtg ggctacttcc      300
tcatcgcagc cggcgttgtg gtctttgctc ttggtttcct gggctgctat ggtgctaaga      360
ctgagagcaa gtgtgccctc gtgacgttct tcttcaccc cctcctcatc ttcattgctg      420
aggttgagc tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt      480
tgctggtagt gcctgccatc aagaaagatt atggttccca ggaagacttc actcaagtgt      540
ggaacaccac catgaaaggg ctcaagtgtc gtggcttcac caactatacg gattttgagg      600
actcacccta cttcaaagag aacagtgcct tccccccatt ctgttgcaat gacaacgtca      660
ccaacacagc caatgaaacc tgcaccaagc aaaaaggctc cgacaaaaa gtagagggtt      720
gcttcaatca gcttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag      780
ctggaattgg gggcctcgag ctggctgcca tgattgtgtc catgtatctg tactgcaatc      840
tacaataagt ccacttctgc ctctgccact actgctgcca catgggaact gtgaagaggc      900
accctggcaa gcagcagtga ttgggggagg ggacaggatc taacaatgtc acttgggcca      960
gaatggacat gccctttctg ctccagactt ggggctagat agggaccact ccttttagcg     1020
atgctgactt ttccttccat tgggtgggtgg atgggtgggg ggcatccag agcctctaag     1080
gtagccagtt ctgttgccca tccccccagt ctattaaacc cttgatatgc cccctaggcc     1140
tagtgggtgat cccagtgtc tactggggga tgagagaaag gcattttata gcctgggcac     1200
aagtgaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc     1260
tgttacaatg ttaaaaaaaa aaaaaaaaaa                                     1289

```

&lt;210&gt; 112

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 112

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1          5          10          15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
          20          25          30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
          35          40          45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
          50          55          60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
          65          70          75          80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
          85          90          95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
          100          105          110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
          115          120          125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
          130          135          140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
          145          150          155          160
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
          165          170          175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
          180          185          190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu

```

```

      195              200              205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
  210              215              220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
  225              230              235              240
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
      245              250              255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
      260              265              270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
      275              280              285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
      290              295              300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
  305              310              315

```

&lt;210&gt; 113

&lt;211&gt; 553

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 113

```

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
  1              5              10              15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
      20              25              30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
      35              40              45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
      50              55              60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
      65              70              75              80
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
      85              90              95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
      100              105              110
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
      115              120              125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
      130              135              140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
      145              150              155              160
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
      165              170              175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
      180              185              190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
      195              200              205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
      210              215              220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
      225              230              235              240
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
      245              250              255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg

```

260 265 270  
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400  
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
 530 535 540  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545 550

&lt;210&gt; 114

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 114

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
 20 25 30  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
 35 40 45  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
 50 55 60  
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65 70 75 80  
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile

```

      85              90              95
Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
      100              105              110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
      115              120              125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
      130              135              140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
      145              150              155              160
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
      165              170              175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
      180              185              190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
      195              200              205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
      210              215              220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
      225              230              235              240
Gln

```

```

<210> 115
<211> 366
<212> DNA
<213> Homo sapien

```

```

<400> 115
gctctttctc tcccctctc tgaatttaat tctttcaact tgcaatttgc aaggattaca      60
catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac      120
ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga      180
actggttagaa aaacatctga agagctagtc tatcagcatc tgacagggtga attggatggg      240
tctcagaacc atttcaccca gacagcctgt ttctatcctg tttataaat tagtttgggt      300
tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt      360
ttagtc                                         366

```

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<210> 116
<211> 282
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (282)
<223> n = A,T,C or G

<400> 116
acaaagatga accatttcct atattatagc aaaattaaaa tctaccgcga ttctaattatt      60
gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa      120
agactttact attttcatat tttaagacac atgatttatc ctatttttagt aacctgggtc      180
atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt      240
tcaatctnga actatctana tcacagacat ttctattcct tt                                         282

```

```

<210> 117
<211> 305

```



<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(305)

<223> n = A,T,C or G

<400> 117

acacatgtcg cttcactgcc ttcttagatg cttctgggtca acatanagga acagggacca	60
tattttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa	120
aataaggcaa aatatatgaa acaacagggtc tcgagatatt ggaaatcagt caatgaagga	180
tactgatccc tgatcactgt cctaatagcag gatgtgggaa acagatgagg tcacctctgt	240
gactgccccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat	300
tgggt	305

<210> 118

<211> 71

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(71)

<223> n = A,T,C or G

<400> 118

accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa	60
aantcctggg t	71

<210> 119

<211> 212

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(212)

<223> n = A,T,C or G

<400> 119

actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca	60
gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac	120
agtaagctgg cccttctaataaaaagaaaat tgaaagggtt ctcactaanc ggaattaant	180
aatggantca aganactccc aggcctcagc gt	212

<210> 120

<211> 90

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(90)

<223> n = A,T,C or G

<400> 120  
actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tggctcttgcc 60  
ctccgccggc gcagaacatg ctgggggtggt 90

<210> 121  
<211> 218  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(218)  
<223> n = A,T,C or G

<400> 121  
tgtancgtga anacgacaga nagggttgtc aaaaatggag aanccttgaa gtcattttga 60  
gaataagatt tgctaaaaga tttggggcta aaacatgggt attgggagac atttctgaag 120  
atatncangt aaattangga atgaattcat ggttcttttg ggaattcctt tacgatngcc 180  
agcatanact tcatgtgggg atancagcta cccttgta 218

<210> 122  
<211> 171  
<212> DNA  
<213> Homo sapien

<400> 122  
taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg 60  
catttgtagt ctcatggaac aggaagtcgg atgggtggggc atcttcagtg ctgcatgagt 120  
caccaccccg gcggggtcat ctgtgccaca ggtccctgtt gacagtgcgg t 171

<210> 123  
<211> 76  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(76)  
<223> n = A,T,C or G

<400> 123  
tgtagcgtga agacnacaga atgggtgtgtg ctgtgctatc caggaacaca tttattatca 60  
ttatcaanta ttgtgt 76

<210> 124  
<211> 131  
<212> DNA  
<213> Homo sapien

<400> 124  
acctttcccc aaggccaatg tcctgtgtgc taactggccg gctgcaggac agctgcaatt 60  
caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg 120  
ttaagatttg t 131

<210> 125  
 <211> 432  
 <212> DNA  
 <213> Homo sapien

<400> 125  
 actttatcta ctggctatga aatagatggt ggaaaattgc gttaccaact ataccactgg 60  
 cttgaaaaag aggtgatagc tcttcagagg acttgtgact tttgtcaga tgctgaagaa 120  
 ctacagtctg catttggcag aaatgaagat gaatttgat taaatgagga tgctgaagat 180  
 ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg 240  
 ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc 300  
 catggtgggg gtcttgcacg tgaagaatg gaattgattt tgcttttgca agaattctag 360  
 caggaaacat cagaaccact attttctagc cctctgtcag agcaaaccctc agtgcctctc 420  
 ctctttgctt gt 432

<210> 126  
 <211> 112  
 <212> DNA  
 <213> Homo sapien

<400> 126  
 acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60  
 agtaagaatg atatttcccc ccagggatca ccaaataatt ataaaaattt gt 112

<210> 127  
 <211> 54  
 <212> DNA  
 <213> Homo sapien

<400> 127  
 accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128  
 <211> 323  
 <212> DNA  
 <213> Homo sapien

<400> 128  
 acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc 60  
 acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca 120  
 ttctctctga agtctagggt acccattttg gggacccatt ataggcaata aacacagttc 180  
 ccaaagcatt tggacagttt ctgtttgtgt tttagaatgg ttttcctttt tcttagcctt 240  
 ttcttgcaaa aggctcactc agtcccttgc ttgctcagtg gactgggctc cccagggcct 300  
 aggctgcctt cttttccatg tcc 323

<210> 129  
 <211> 192  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(192)  
 <223> n = A,T,C or G

<400> 129  
acatacatgt gtgtatatatt ttaaatatca cttttgtatc actctgactt tttagcatac 60  
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc 120  
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg 180  
gataaacaaa gt 192

<210> 130

<211> 362

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(362)

<223> n = A,T,C or G

<400> 130  
ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60  
tataatgacg caacaaaaag gtgctgttta gtcctatggt tcagtttatg cccctgacaa 120  
gtttccattg tgttttgccg atcttctggc taatcgtggt atcctccatg ttattagtaa 180  
ttctgtattc cattttgcta acgcctggta gatgtaacct gctangaggc taactttata 240  
cttatttaaa agctcttatt ttgtgggtcat taaaatggca atttatgtgc agcactttat 300  
tgcagcagga agcacgtgtg gggtgggtgt aaagctcttt gctaattctta aaaagtaatg 360  
gg 362

<210> 131

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 131  
ctttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca 60  
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga 120  
gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc 180  
ttctgaacta gattaaggca gcttgtaa atctgatgtgat ttggtttatt atccaactaa 240  
cttccatctg ttatcactgg agaaagccca gactccccan gacnggtacg gattgtgggc 300  
atanaaggat tgggtgaagc tggcgttgtg gt 332

<210> 132

<211> 322

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(322)

<223> n = A,T,C or G

<400> 132  
acttttgcca ttttgtatat ataaacaatc ttgggacatt ctcttgaaaa ctaggtgtcc 60

```

agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat   120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt   180
tttagcaagt taaaatgaan atgacaggaa aggccttattt atcaacaaag agaagagttg   240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct   300
gtaacaatct acaattgggc ca                                     322

```

<210> 133

<211> 278

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 133

```

acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt   60
cttgtttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta   120
ctatttaaaa aaaatcacia atctttccct ttaagctatg ttnaattcaa actattcctg   180
ctattcctgt ttgtcaaag aaattatatt ttctaaaata tgtntatttg tttgatgggt   240
cccacgaaac actaataaaa accacagaga ccagcctg                               278

```

<210> 134

<211> 121

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(121)

<223> n = A,T,C or G

<400> 134

```

gtttanaaaa cttgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca   60
tgattctctg aggttaaact tggttttcaa atgttatatt tacttgtatt ttgcttttgg   120
t                                                         121

```

<210> 135

<211> 350

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(350)

<223> n = A,T,C or G

<400> 135

```

acttanaacc atgacctagca catcagaatc cctcaaagaa catcagtata atcctataacc   60
atancaagtg gtgactgggt aagcgtgcga caaagggtcag ctggcacatt acttgtgtgc   120
aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca   180
gggtgcccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgct   240
ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag   300
ttcccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt               350

```

<210> 136  
 <211> 399  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(399)  
 <223> n = A,T,C or G

<400> 136  
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60  
 gctgtgattg tatccgaata ntccctcgtga gaaaagataa tgagatgacg tgagcagcct 120  
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180  
 cctggcggcc agccagccag ccacagggtg gcttcttctt tttgtggtga caacnccaag 240  
 aaaactgcag agggccaggg tcagggtgtna gtgggtangt gaccataaaa caccagggtgc 300  
 tcccaggaac ccggggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360  
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137  
 <211> 165  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(165)  
 <223> n = A,T,C or G

<400> 137  
 actggtgtgg tngggggtga tgctgggtgt anaagttgan gtgacttcan gatggtgtgt 60  
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120  
 ttggctggtc ccaactggtg tcaactgtcat tgggtggggtt cctgt 165

<210> 138  
 <211> 338  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(338)  
 <223> n = A,T,C or G

<400> 138  
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60  
 ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccac 120  
 tgctgggcag tctcccatgc cttccacagt gaaagggctt gagaaaaatc acatccaatg 180  
 tcatgtgttt ccagccacac caaaagggtg ttggggtgga gggctggggg catananggt 240  
 cangectcag gaagcctcaa gtccattca gctttgccac tgtacattcc ccatntttaa 300  
 aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139  
 <211> 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 139

gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa	60
gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccga gtgaaggaga	120
attcaaacag acctcgatcat tcctgggtgtg agcctggctg gctcaccgcc tatcatctgc	180
atttgcctta ctcaggtgct accggactct ggcccctgat gtctgtagtt tcacaggatg	240
ccttatttgt cttctacacc ccacagggcc cctacttct tcggatgtgt ttttaataat	300
gtcagctatg tgcccatcc tccttcatgc cctccctccc tttcctacca ctgctgagtg	360
gcctggaact tgtttaaagt gt	382

&lt;210&gt; 140

&lt;211&gt; 200

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(200)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 140

accaaantct ctttctgttg tgttngattt tactataggg gtttngcttn ttctaaanat	60
acttttcatt taacancttt tgtaagtgt caggctgcac tttgtccat anaattattg	120
ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt	180
atattcagca taaaggagaa	200

&lt;210&gt; 141

&lt;211&gt; 335

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(335)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 141

actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggtgg	60
gggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc agggtttggt	120
atgcatgtag agaaccctaaa ctaatttatt aaacaggata gaaacaggct gtctgggtga	180
aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg	240
tttttctacc agttcagaga tnggttaatg actantcca atggggaaaa agcaagatgg	300
attcacaac caagtaattt taaacaaaga cactt	335

&lt;210&gt; 142

&lt;211&gt; 459

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(459)

&lt;223&gt; n = A,T,C or G

<400> 142  
accagggttaa tattgccaca tatatccttt ccaattgcgg gctaaacaga cgtgtattta 60  
gggttggtta aagacaaccc agcttaatat caagagaaat tgtgacctt catggagtat 120  
ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca 180  
cacatggtcc aacaacactc aaataataaa tcaaataatna tcagatgta aagattgggc 240  
ttcaaacatc atagccaatg atgccccgct tgccataat ctctccgaca taaaaccaca 300  
tcaacacctc agtggccacc aaaccattca gcacagcttc cttaactgtg agctggttga 360  
agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct 420  
cagcanggggt gggaggaacc agtcaacct tggcgctant 459

<210> 143  
<211> 140  
<212> DNA  
<213> Homo sapien

<400> 143  
acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg 60  
aaatccaac agtctctcct agaaaggaat agtgtcacca accccacca tctccctgag 120  
accatccgac ttcctgtgt 140

<210> 144  
<211> 164  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (164)  
<223> n = A,T,C or G

<400> 144  
acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60  
atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta tacaaatttg 120  
aggcaattaa tccatatttg ttttcaataa ggaaaaaag atgt 164

<210> 145  
<211> 303  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (303)  
<223> n = A,T,C or G

<400> 145  
acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa 60  
actggagggt atttatacc c aattatccca ttcattaaca tgccctcctc ctcaggctat 120  
gcaggacagc tatcataagt cggcccaggc atccagatac taccatttgt ataaacttca 180  
gtaggggagt ccatccaagt gacaggctca atcaaaggag gaaatggaac ataagcccag 240  
tagtaaaatn ttgcttagct gaaacagcca caaaaagactt accgcccgtg tgattaccat 300  
caa 303

<210> 146



<211> 327  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(327)  
<223> n = A,T,C or G

<400> 146  
actgcagctc aattagaagt ggtctctgac ttctcatcanc ttctccctgg gctccatgac 60  
actggcctgg agtgactcat tgctctgggtt ggttgagaga gctcctttgc caacaggcct 120  
ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180  
cctgaacagg gaggggtggga ggagccagca tggaacaagc tgccactttc taaagtagcc 240  
agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300  
taggggtgag ctgtgtgact ctatggt 327

<210> 147  
<211> 173  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(173)  
<223> n = A,T,C or G

<400> 147  
acattgtttt tttgagataa agcattgana gagctctcct taacgtgaca caatggaagg 60  
actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120  
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148  
<211> 477  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(477)  
<223> n = A,T,C or G

<400> 148  
acaaccactt tatctcatcg aattttttaac ccaaactcac tcactgtgcc tttctatcct 60  
atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120  
gccctactac ctgctgcaat aatcacattc ccttcctgtc ctgaccctga agccattggg 180  
gtggtcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgctcac 240  
nccanccac ctcaccgacc ccatcctctt acacagctac ctccctgtct tctaacccca 300  
tagattatnt ccaaattcag tcaattaagt tactattaac actctacccg acatgtccag 360  
caccactggt aagccttctc cagccaacac acacacacac acacncacac acacacatat 420  
ccaggcacag gctacctcat cttcacaatc acccctttaa ttaccatgct atggtgg 477

<210> 149  
<211> 207  
<212> DNA

<213> Homo sapien

<400> 149

```
acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac      60
taacgtatatt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct      120
gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca      180
tttcaggcag agggaacagc agtgaaa                                           207
```

<210> 150

<211> 111

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(111)

<223> n = A,T,C or G

<400> 150

```
accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg      60
cacttaaatg tggtcagtgt ttggacttgt taactantgg catctttggg t                111
```

<210> 151

<211> 196

<212> DNA

<213> Homo sapien

<400> 151

```
agcgcggcag gtcatttga acattccaga tacctatcat tactcgatgc tgttgataac      60
agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat      120
ggataccaac cggaaaaccc ctatcccgca cagcccactg tggccccac tgtctacgag      180
gtgcatccgg ctcagt                                                         196
```

<210> 152

<211> 132

<212> DNA

<213> Homo sapien

<400> 152

```
acagcacttt cacatgtaag aaggagaaaa ttcctaaatg taggagaaaag ataacagaac      60
cttccccctt tcatctagtg gtggaaacct gatgctttat gttgacagga atagaaccag      120
gagggagttt gt                                                         132
```

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(285)

<223> n = A,T,C or G

<400> 153

```
acaanaccca nganaggcca ctggccgtgg tgatcatggcc tccaaacatg aaagtgtcag      60
```

cttctgctct	tatgtcctca	tctgacaact	ctttaccatt	tttatcctcg	ctcagcagga	120
gcacatcaat	aaagtccaaa	gtcttggaact	tggccttggc	ttggagggaag	tcatacaacac	180
cctggctagt	gagggtgcgg	cgccgctcct	ggatgacggc	atctgtgaag	tcgtgcacca	240
gtctgcaggc	cctgtggaag	cgccgtccac	acggagtnag	gaatt		285

&lt;210&gt; 154

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 154

accacagtcc	tgttggggcca	gggcttcatg	accctttctg	tgaaaagcca	tattatcacc	60
accccaaat	tttccttaaa	tatctttaac	tgaaggggtc	agcctcttga	ctgcaaagac	120
cctaagccgg	ttacacagct	aactcccact	ggccctgatt	tgtgaaattg	ctgctgcctg	180
attggcacag	gagtcgaagg	tgttcagctc	ccctcctccg	tggaaacgaga	ctctgatttg	240
agtttcacaa	attctcgggc	cacctcgtea	ttgtcctctt	gaaataaaat	ccggagaatg	300
gtcaggcctg	tctcatccat	atggatcttc	cgg			333

&lt;210&gt; 155

&lt;211&gt; 308

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(308)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 155

actggaaata	ataaaaccca	catcacagt	ttgtgtcaaa	gatcatcagg	gcatggatgg	60
gaaagtgtt	tgggaactgt	aaagtgccta	acacatgata	gatgattttt	gttataatat	120
ttgaatcacg	gtgcatacaa	actctcctgc	ctgtcctccc	tgggccccag	ccccagcccc	180
atcacagctc	actgctctgt	tcatccaggc	ccagcatgta	gtggctgatt	cttcttggct	240
gcttttagcc	tccanaagtt	tctctgaagc	caaccaaacc	tctangtgta	aggcatgctg	300
gccctggg						308

&lt;210&gt; 156

&lt;211&gt; 295

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 156

accttgctcg	gtgcttggaa	catattagga	actcaaaata	tgagatgata	acagtgccta	60
ttattgatta	ctgagagaac	tgtagacat	ttagttgaag	attttctaca	caggaaactga	120
gaataggaga	ttatgtttgg	ccctcatatt	ctctcctatc	ctccttgctt	cattctatgt	180
ctaatatatt	ctcaatcaaa	taaggtttagc	ataatcagga	aatcgaccaa	ataccaatat	240
aaaaccagat	gtctatcctt	aagattttca	aatagaaaac	aaattaacag	actat	295

&lt;210&gt; 157

&lt;211&gt; 126

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 157

acaagtttaa	atagtgtgt	cactgtgcat	gtgctgaaat	gtgaaatcca	ccacatttct	60
------------	-----------	------------	------------	------------	------------	----

gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc 120  
cttagt 126

<210> 158

<211> 442

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(442)

<223> n = A,T,C or G

<400> 158

acccactggg cttggaaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg 60  
aanccagcag gctgccccta gtcagtcctt ccttccagag aaaaagagat ttgagaaagt 120  
gcctgggtaa ttcaccatta atttcctccc ccaaactctc tgagtcttcc cttaatattt 180  
ctggtgggttc tgaccaaagc aggtcatggg ttggtgagca tttgggatcc cagtgaagta 240  
natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtgg cagagtgggtg 300  
ccaaccctgt tttccagtc cacgtagaca gattcacagt gcggaattct ggaagctgga 360  
nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg 420  
tgttcattct ctgatgtcct gt 442

<210> 159

<211> 498

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(498)

<223> n = A,T,C or G

<400> 159

acttccaggt aacgttggtt tttccgttga gcctgaactg atgggtgacg ttgtagggtc 60  
tccaacaaga actgagggtt cagagcgggt aggggaagagt gctgttccag ttgcacctgg 120  
gctgctgtgg actgttggtt attcctcact acggcccaag gttgtggaac tggcanaaag 180  
gtgtgttgtt gganttgagc tcgggcgggt gtggtagggt gtgggctctt caacaggggc 240  
tgctgtgggt ccgggagtg aangtggtgt gtcacttgag cttggccagc tctggaaagt 300  
antanattct tcctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa 360  
cgaaccagtg ctgctgtggg tgggtgtana tcctccacaa agcctgaagt tatggtgtcn 420  
tcaggtaana atgtgggttc agtgtccctg ggcngctgtg gaaggttgta nattgtcacc 480  
aagggaataa gctgtggg 498

<210> 160

<211> 380

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(380)

<223> n = A,T,C or G

<400> 160

```

acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac      60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct      120
ggagcatggc atagaggaag ctganaaatg tgggggtctga ggaagccatt tgagtctggc      180
cactagacat ctcacagcc acttggtgta agagatgccc catgaccca gatgcctctc      240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg      300
gagaaaaatg gcagtttgac cgaacctgtt cacaacggta gaggctgatt tctaacgaaa      360
cttgtagaat gaagcctgga

```

```

<210> 161
<211> 114
<212> DNA
<213> Homo sapien

```

```

<400> 161
actccacatc ccctctgagc aggcgggtgt cgttcaaggt gtatttggcc ttgcctgtca      60
cactgtccac tggcccctta tccacttggt gcttaatccc tcgaaagagc atgt          114

```

```

<210> 162
<211> 177
<212> DNA
<213> Homo sapien

```

```

<400> 162
actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa      60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt      120
tggtgatata taacttggca ataaccagct ctggtgatac ataaaactac tcaactgt      177

```

```

<210> 163
<211> 137
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(137)
<223> n = A,T,C or G

```

```

<400> 163
catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac      60
canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt      120
catcagcggc atgatgt

```

```

<210> 164
<211> 469
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(469)
<223> n = A,T,C or G

```

```

<400> 164
cttatcacia tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta      60
tgcaatgcat catgctatct catacctaag gagggagtgc caggagattc aaccaggaaa      120

```

```

tgcattggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt      180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg      240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg      300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct      360
tctagtaggc acagggctcc caggccaggc ctcattctcc tctggcctct aatagtcaat      420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt      469

```

&lt;210&gt; 165

&lt;211&gt; 195

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(195)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 165

```

acagtttttt atanatatcg acattgccgg cacttggtgt cagtttcata aagctgggtg      60
atccgctgtc atccactatt ccttggttag agtaaaaatt attcttatag cccatgtccc      120
tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact      180
tcctctgaga tgagt      195

```

&lt;210&gt; 166

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(383)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 166

```

acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc      60
cgaggtcgga gtccacacca ccggtgtagg tgtgtcfaat cttgggcttg gcgcccacct      120
ttggagaagg gatatgtgca acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt      180
tttgagacc agcctgagca aggggcggat gttcagcttc agtcctcctc tcgtcaggtg      240
gatgccaaac tcgtctangg tccgtgggaa gctgggtgtc acntcaccta caacctgggc      300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt      360
nggggccttt ttggtgaact ttc      383

```

&lt;210&gt; 167

&lt;211&gt; 247

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(247)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 167

```

acagagccag accttggcca taaatgaanc agagattaag actaaacccc aagtcganat      60
tggagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc      120

```

tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac	180
tcaatctgan tccaaagtgg tggctggaac actggtcatg acanaggcag tgactctgac	240
tgangtc	247

&lt;210&gt; 168

&lt;211&gt; 273

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(273)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 168

acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa	60
aatccctcan ccttggttctt cacnactgtc tatactgana gtgtcatggt tccacaaagg	120
gctgacacct gagcctgnat tttcactcat ccctgagaag ccctttccag taggggtgggc	180
aattcccaac ttccttgcca caagcttccc aggctttctc ccctggaaaa ctccagcttg	240
agtcccagat acactcatgg gctgccctgg gca	273

&lt;210&gt; 169

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(431)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 169

acagccttgg cttccccaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc	60
agctcagacc aggggtcaaag gatgtgacat caacagtttc tggtttcaga acaggttcta	120
ctactgtcaa atgaccccc atacttctc aaaggctgtg gtaagttttg cacagggtgag	180
ggcagcagaa aggggggtant tactgatgga caccatcttc tctgtatact ccacactgac	240
cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcaactgctgg gcaccagctc	300
acgcacatca ctgacaaccg ggatggaaaa agaantgcc aactttcatat atccaactgg	360
aaagtgatct gatactggat tcttaattac cttcaaaagc ttctgggggc catcagctgc	420
tcgaacactg a	431

&lt;210&gt; 170

&lt;211&gt; 266

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(266)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 170

acctgtgggc tgggctgtta tgcctgtgcc ggctgctgaa agggagttca gaggtggagc	60
tcaaggagct ctgcaggcat tttgccaanc ctctccanag canagggagc aacctacact	120
ccccgctaga aagacaccag attggagtcc tgggaggggg agttgggggtg ggcatttgat	180

gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240  
tcaaagctag gggctctggca ggtgga 266

<210> 171  
<211> 1248  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(1248)  
<223> n = A,T,C or G

<400> 171  
ggcagccaaa tcataaacgg cgaggactgc agcccgact cgcagccctg gcaggcggca 60  
ctgggtcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcattccgca gtgggtgctg 120  
tcagccgcac actgtttcca gaagtgaagt cagagctcct acaccatcgg gctgggcctg 180  
cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta 240  
cggcaccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac 300  
gaatccgtgt ccgagctga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360  
gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420  
gtgctgcagt gcgtgaacgt gtcggtggtg tctgaggagg tctgcagtaa gctctatgac 480  
ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc 540  
aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtctttc 600  
ggaaaagccc cgtgtggcca agttggcgtg ccagggtgtct acaccaacct ctgcaaattc 660  
actgagtggg tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa 720  
attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agcccctcct 780  
ccctcaggcc caggagtcca ggccccagc cctcctccc tcaaaccaag ggtacagatc 840  
cccagcccct cctccctcag acccaggagt ccagaccccc cagccccctc tccctcagac 900  
ccaggagtcc agcccctcct ccctcagacc caggagtcca gacccccag cccctcctcc 960  
ctcagaccca ggggtccagg cccccaacct ctctcctc agactcagag gtccaagccc 1020  
ccaaccntc attccccaga cccagaggtc cagggtcccag cccctntcc ctcagaccca 1080  
gcgggtccaat gccacctaga ctntccctgt acacagtgcc ccttggtggc acgttgaccc 1140  
aaccttacca gttggttttt catttttngt ccctttcccc tagatccaga aataaagttt 1200  
aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1248

<210> 172  
<211> 159  
<212> PRT  
<213> Homo sapien

<220>  
<221> VARIANT  
<222> (1)...(159)  
<223> Xaa = Any Amino Acid

<400> 172  
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro  
1 5 10 15  
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser  
20 25 30  
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr  
35 40 45  
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly  
50 55 60



Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu  
 65 70 75 80  
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe  
 85 90 95  
 Cys Ala Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser  
 100 105 110  
 Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe  
 115 120 125  
 Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn  
 130 135 140  
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 145 150 155

<210> 173

<211> 1265

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(1265)

<223> n = A,T,C or G

<400> 173

ggcagcccg	actcgagcc	ctggcaggcg	gcactgggtca	tggaaaacga	attgttctgc	60
tcgggctcc	tgggtgcatcc	gcagtgggtg	ctgtcagccg	cacactgttt	ccagaactcc	120
tacaccatcg	ggctgggcct	gcacagtctt	gaggccgacc	aagagccagg	gagccagatg	180
gtggaggcca	gcctctccgt	acggcaccca	gagtacaaca	gaccttgc	cgctaacgac	240
ctcatgctca	tcaagttgga	cgaatccgtg	tccgagtc	acaccatccg	gagcatcagc	300
attgcttcgc	agtgcctac	cgcggggaac	tcttgccctc	tttctggctg	gggtctgctg	360
gcgaacggtg	agctcacggg	tgtgtgtctg	ccctcttcaa	ggaggtcctc	tgcccagtcg	420
cgggggctga	cccagagctc	tgcgtcccag	gcagaatgcc	taccgtgctg	cagtgcgtga	480
acgtgtcgg	ggtgtctgag	gaggtctgca	gtaagctcta	tgacccgctg	taccaccca	540
gcatgttctg	cgccggcgga	gggcaagacc	agaaggactc	ctgcaacggg	gactctgggg	600
ggcccctgat	ctgcaacggg	tacttgacag	gccttgtgtc	tttcggaaaa	gccccgtgtg	660
gccaaagtgg	cgtgccaggt	gtctacacca	acctctgcaa	attcactgag	tggatagaga	720
aaaccgtcca	ggccagttaa	ctctggggac	tgggaaccca	tgaaattgac	ccccaaatac	780
atcctgcgga	aggaattcag	gaatatctgt	tcccagcccc	tcctccctca	ggcccaggag	840
tccaggcccc	cagcccctcc	tccctcaaac	caagggtaca	gatccccagc	ccctcctccc	900
tcagaccag	gagtcagac	ccccagccc	ctcctccctc	agacccagga	gtccagcccc	960
tcctcctca	gacccaggag	tccagacccc	ccagccccctc	ctccctcaga	cccaggggtt	1020
gaggccccca	accctcctc	cttcagagtc	agagggtccaa	gcccccaacc	cctcgttccc	1080
cagaccacaga	ggttnnaggtc	ccagccccctc	ttccntcaga	cccagnngtc	caatgccacc	1140
tagattttcc	ctgnacacag	tgcccccttg	tggngangttg	acccaacctt	accagttggg	1200
ttttcatttt	tngtcccttt	cccctagatc	cagaaataaa	gtttaagaga	ngngcaaaaa	1260
aaaaa						1265

<210> 174

<211> 1459

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(1459)

<223> n = A,T,C or G

<400> 174

```

ggtcagccgc acactgtttc cagaagtgag tgcagagctc ctacaccatc gggctggggc 60
tgcacagtct tgaggccgac caagagccag ggagccagat ggtggaggcc agcctctccg 120
tacggcaccc agagtacaac agacccttgc tcgctaacga cctcatgctc atcaagttgg 180
acgaatccgt gtccgagtct gacaccatcc ggagcatcag cattgcttcg cagtgcctta 240
ccgcggggaa ctcttgctc gtttctggct ggggtctgct ggcgaacggt gagctcacgg 300
gtgtgtgtct gccctcttca aggaggtcct ctgcccagtc gcgggggctg acccagagct 360
ctgcgtccca ggcagaatgc ctaccgtgct gcagtgcgtg aacgtgtcgg tgggtgtctga 420
ngaggtctgc antaagctct atgaccgct gtaccacccc ancatgttct gcgccggcgg 480
agggcaagac cagaaggact cctgcaacgt gagagagggg aaaggggagg gcaggcgact 540
cagggaaagg tggagaaggg ggagacagag acacacaggg ccgcatggcg agatgcagag 600
atggagagac acacagggag acagtgacaa cttagagagag aaactgagag aaacagagaa 660
ataaacacag gaataaagag aagcaaagga agagagaaac agaaacagac atggggaggc 720
agaaacacac acacatagaa atgcagttga ccttccaaca gcatggggcc tgagggcggt 780
gacctccacc caatagaaaa tcctcttata acttttgact ccccaaaaac ctgactagaa 840
atagcctact gttgacgggg agccttacca ataacataaa tagtcgattt atgcatacgt 900
tttatgcatt catgatatac ctttgttga atttttggat atttctaagc tacacagttc 960
gtctgtgaat ttttttaaat tgttgcaact ctccataaat ttttctgatg tgtttattga 1020
aaaaatccaa gtataagtgg acttgtgcat tcaaaccagg gttgttcaag ggtcaactgt 1080
gtaccagag ggaacagtg acacagattc atagaggtga aacacgaaga gaaacaggaa 1140
aaatcaagac tctacaaaga ggctgggcag ggtggctcat gcctgtaatc ccagcacttt 1200
gggaggcgag gcaggcagat cacttgaggt aaggagttca agaccagcct ggccaaaatg 1260
gtgaaatcct gtctgtacta aaaatacaaa agttagctgg atatggtggc aggcgcctgt 1320
aatcccagct acttgggagg ctgaggcagg agaattgctt gaatatggga ggcagaggtt 1380
gaagtgagtt gagatcacac cactatactc cagctggggc aacagagtaa gactctgtct 1440
caaaaaaaaa aaaaaaaaaa
1459

```

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(1167)

<223> n = A,T,C or G

<400> 175

```

gcgcagccct ggcaaggcggc actggtcatg gaaaacgaat tgttctgctc gggcgtcctg 60
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg 120
ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc 180
ctctccgtac ggcacccaga gtacaacaga ctcttgctcg ctaacgacct catgctcatc 240
aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgcag 300
tgccctaccg cggggaactc ttgcctcgtn tctggctggg gtctgctggc gaacggcaga 360
atgcctaccg tgctgcaact cgtgaacgtg tcggtggtgt ctgaggangt ctgcagtaag 420
ctctatgacc cgctgtacca ccccagcatg ttctgcgccg gcggagggca agaccagaag 480
gactcctgca acggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt 540
gtgtctttcg gaaaagcccc gtgtggccaa cttggcgtgc caggtgtcta caccaacctc 600
tgcaaattca ctgagtggat agagaaaacc gtccagncca gtttaactctg gggactggga 660
accatgaaa ttgaccccca aatacatcct gcggaangaa ttcaggaata tctgttccca 720
gccccctcct cctcaggccc aggagtccag gccccagcc cctctccct caaaccaagg 780
gtacagatcc ccagcccctc ctccctcaga cccaggagtc cagaccccc agccctcnt 840
ccntcagacc caggagtcca gccccctcct cntcagacgc aggagtccag accccccagg 900

```

```

ccntcntccg tcagacccag ggggtgcaggc ccccaacccc tcntccntca gagtcagagg      960
tccaagcccc caaccctcg ttccccagac ccagaggtnc aggtcccagc cctcctccc      1020
tcagacccag cggccaatg ccacctagan tntccctgta cacagtgcc ccttggtggca      1080
ngttgaccca accttaccag ttggtttttc attttttgtc cctttcccct agatccagaa      1140
ataaagtnta agagaagcgc aaaaaaa      1167

```

&lt;210&gt; 176

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(205)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 176

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
 50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
100          105          110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
115          120          125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
130          135          140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
145          150          155          160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
165          170          175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
180          185          190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
195          200          205

```

&lt;210&gt; 177

&lt;211&gt; 1119

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 177

```

gcgcactcgc agccctggca ggcggcactg gtcattgaaa acgaattggt ctgctcgggc      60
gtcctgggtgc atccgcagtg ggtgctgtca gccgcacact gttccagaa ctcctacacc      120
atcgggctgg gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag      180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct      300

```

```

tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctgggggtct gctgggcgaac 360
gatgctgtga ttgccatcca gtcccagact gtgggagggt gggagtgtga gaagctttcc 420
caaccctggc aggggtgtac catttcggca acttccagtg caaggacgtc ctgctgcac 480
ctcactgggt gctcactact gctcactgca tcacccggaa cactgtgatc aactagccag 540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc 720
tgacctacag aggtgagggg tcatatagct cttcaaggat gctggtactc ccctcacaaa 780
ttcattttctc ctggtgtagt gaaagggtgcg ccctctggag cctcccaggg tgggtgtgca 840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttta atccctcatg 900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca 960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg 1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc 1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaaa 1119

```

&lt;210&gt; 178

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1) ... (164)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 178

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1           5           10           15
Val Leu Ser Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
      20           25           30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
      35           40           45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
      50           55           60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
      65           70           75           80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
      85           90           95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
      100          105          110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
      115          120          125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
      130          135          140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
      145          150          155          160
Pro Gly Thr Leu

```

&lt;210&gt; 179

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 179

ctggagtgcc ttggtgtttc aagccccctgc aggaagcaga atgcaccttc tgaggcacct	60
ccagctgccc ccggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct	120
gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga	180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa	240
aaaaaaaa	250

&lt;210&gt; 180

&lt;211&gt; 202

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 180

actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca	60
tcaccagac ccgcccctg cccgtgcccc acgtgctgc taacgacagt atgatgctta	120
ctctgctact cggaaactat ttttatgtaa ttaatgtatg ctttcttgtt tataaatgcc	180
tgatttaaaa aaaaaaaaaa aa	202

&lt;210&gt; 181

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(558)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 181

tccytttgkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg	60
aatgtttagg cagtgctagt aatttcytcg taatgattct gttattactt tcctnattct	120
ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa	180
ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca	240
aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaac	300
ctactctgtt ccttggctag aaaaaattat aaacaggact ttgttagttt gggaagccaa	360
attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw	420
ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt	480
aaaaycagtt ttggtwaata ygtwaatatg tcmtaataaa acaakgcttt gacttatttc	540
caaaaaaaaa aaaaaaaa	558

&lt;210&gt; 182

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(479)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 182

acagggwttk grggatgcta agsccccrga rwtggtttga tccaaccctg gcttwttttc	60
agaggggaaa atggggccta gaagttacag mscatytagy tgggtcgmtg gcaccctcg	120
cstcacacag astcccagat agctgggact acaggcacac agtcaactgaa gcaggccctg	180
ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca	240
ctaagggttaa actttccac ccagaaaagg caacttagat aaaatcttag agtactttca	300

tactmttcta agtcctcttc cagcctcact kkgagtcctm cytggggggtt gataggaant	360
ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttg tacgcatara	420
awtgstgara aaattaaaaat gttctgggty mactttaaaa araaaaaaaa aaaaaaaaaa	479

<210> 183  
 <211> 384  
 <212> DNA  
 <213> Homo sapien

<400> 183	
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc	60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtg cttcagtgc	120
ggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt	180
gccagcacca gtggcagctc tgggtgctgt ggtttctcct acaagtgaga ttttagatat	240
tgtaatcct gccagtcttt ctcttcaagc cagggtgcat cctcagaaac ctactcaaca	300
cagcaacta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt	360
gccatttcaa aaaaaaaaaa aaaa	384

<210> 184  
 <211> 496  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(496)  
 <223> n = A,T,C or G

<400> 184	
accgaattgg gaccgctggc ttataagcga tcatgtyynt ccrgtatcac ctcaacgagc	60
agggagatcg agtctatacg ctgaagaaat ttgaccgat gggacaacag acctgctcag	120
ccatcctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga	180
aacgcttcaa ggtgctcatg acccagcaac cgcgccctgt cctctgaggg tcccttaa	240
tgatgtcttt tctgccacct gttaccctc ggagactccg taaccaaact cttcggactg	300
tgagccctga tgcccttttg ccagccatac tctttggcat ccagtctctc gtggcgattg	360
attatgcttg tgtgaggcaa tcatgggtggc atcaccata aagggaacac atttgacttt	420
tttttctcat attttaaat actacmagaw tattwmagaw waaatgawtt gaaaaactst	480
taaaaaaaa aaaaaa	496

<210> 185  
 <211> 384  
 <212> DNA  
 <213> Homo sapien

<400> 185	
gctggtagcc tatggcgkcg cccacggagg ggctcctgag gccacggrac agtgacttcc	60
caagtatcyt gcgcsgegtc ttctaccgtc cctacctgca gatctcggg cagattcccc	120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag cccggctct	180
gggcacaccc tcctggggcc caggcgggca cctgcgtctc ccagtatgcc aactggctgg	240
tgggtgctgt cctcgtcatc ttcctgctcg tggccaacat cctgctggtc aactgctca	300
ttgccatggt cagttacaca ttcggcaaag tacagggcaa cagcgatctc tactgggaag	360
gcgcagcgtt accgcctcat ccgg	384

<210> 186  
 <211> 577

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(577)

<223> n = A,T,C or G

<400> 186

gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cytcctggca	tcttggggcg	gcntaatatt	120
ccaggaaact	ctcaatcaag	tcaccgctga	tgaaacctgt	gggctggttc	tgtcttccgc	180
tcggtgtgaa	aggatctccc	agaaggagtg	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtaccag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgccgttga	mcgtgccgaa	garcaccgag	ccttgtgtgg	gggkkgaaagt	360
ctcaccacaga	ttctgcatta	ccagagagcc	gtggcaaaag	acattgacaa	actcgcccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcctc	gtcmgttggt	ggcagcgctw	480
tccttttgac	acacaaaaca	gttaaaggca	ttttcagccc	ccagaaantt	gtcatcatcc	540
aagatntcgc	acagcactna	tccagttggg	attaaat			577

<210> 187

<211> 534

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(534)

<223> n = A,T,C or G

<400> 187

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctggtattaa	aattcacaat	atgcaacact	120
ttaaacagtg	tgtcaatctg	ctcccyynac	tttgtcatca	ccagtctggg	aakaagggtta	180
tgccctattc	acacctgtta	aaagggcgct	aagcatTTTT	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagtaaac	agttatyaat	ttgttagcca	attcactttc	300
ttcatgggac	agagccatyt	gatttaaaaa	gcaaattgca	taatattgag	cttygggagc	360
tgatatttga	gcggaagagt	agcctttcta	cttcaccaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgttctg	480
aggatctccc	agtttattta	ccacttgcac	aagaaggcgt	tttcttctc	aggc	534

<210> 188

<211> 761

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(761)

<223> n = A,T,C or G

<400> 188

agaaaccagt	atctctnaaa	acaacctctc	ataccttggt	gacctaatTT	tgtgtgcgtg	60
tgtgtgtgcg	cgcataattat	atagacaggc	acatcttttt	tactttttgta	aaagcttatg	120
cctctttggg	atctatatct	gtgaaagttt	taatgatctg	ccataatgtc	ttggggacct	180

```

ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc ctkgackarg      300
ggggacaaaag aaaagcaaaa ctgamcataa raaacaatwa cctggtgaga arttgcataa      360
acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wttctccctt      420
gcaaaaaaaca tgtacngact tcccgttgag taatgccaag ttgttttttt tatnataaaa      480
cttgcccttc attacatggt tnaaagtggg gtgggtggggc aaaatattga aatgatggaa      540
ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac      600
atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta      660
tttttctgtn ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac      720
gaaaataata acattgaaga aaaananaaa aaanaaaaaa a                                761

```

&lt;210&gt; 189

&lt;211&gt; 482

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (482)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 189

```

tttttttttt tttgccgatn ctactatntt attgcaggan gtgggggtgt atgcaccgca      60
caccggggct atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca      120
aagccgcctg ctgccttctc tgtctgtctc ctgggtgcagg cacatgggga gaccttcccc      180
aaggcagggg ccaccagtcc aggggtggga atacaggggg tgggagtgt gcataagaag      240
tgataggcac aggccaccgg gtacagacct ctgggtcctt gacaggtnga tttcgaccag      300
gtcattgtgc cctgcccagg cacagcgtn atctggaaaa gacagaatgc tttccttttc      360
aaatttggct ngtcattgaa ngggcanttt tccaanttng gctnggtcct ggtaaccttg      420
gttcggccca gtcctncgtc caaaaantat tcaccnctt ccnaattgct tgcngncccc      480
cc                                                                482

```

&lt;210&gt; 190

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (471)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 190

```

tttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtgggttttg      60
aaaactctcg catccagtga gaactaccat acaccacatt acagctngga atgtntctca      120
aatgtctggg caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag      180
cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt      240
taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt      300
tgaaaaattt catgtatgca atccaaccaa agaacttnat tgggtgatcat gantnctcta      360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacncngt acaaaaanaa      420
tctgtaattn anttcaacct ccgtacngaa aaatntntnt tataactcc c                                471

```

&lt;210&gt; 191

&lt;211&gt; 402

&lt;212&gt; DNA



<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(402)

<223> n = A,T,C or G

<400> 191

gagggattga	aggctgtgtc	tastgtcggm	ctgttcagcc	accaactcta	acaagttgct	60
gtcttccact	cactgtctgt	aagcttttta	acccagacwg	tatcttcata	aatagaacaa	120
attcttcacc	agtcacatct	tctaggacct	ttttggattc	agttagtata	agctcttcca	180
cttcctttgt	taagacttca	tctggtaaag	tcttaagttt	tgtagaaagg	aattyaattg	240
ctcgttctct	aacaatgtcc	tctccttgaa	gtatttggct	gaacaaccca	cctaaagtcc	300
ctttgtgcat	ccattttaaa	tatacttaat	agggcattgk	tncactaggt	taaattctgc	360
aagagtcac	tgtctgcaaa	agttgcgtta	gtatatctgc	ca		402

<210> 192

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(601)

<223> n = A,T,C or G

<400> 192

gagctcggat	ccaataatct	ttgtctgagg	gcagcacaca	tatncagtgc	catggnaact	60
ggtctacccc	acatgggagc	agcatgccgt	agntatataa	ggtcattccc	tgagtcagac	120
atgcytyttt	gaytaccgtg	tgccaagtgc	tggtgattct	yaacacacyt	ccatcccgyt	180
cttttgtgga	aaaactggca	cttkcttgga	actagcarga	catcacttac	aaattcaccc	240
acgagacact	tgaaggtgt	aacaaagcga	ytcttgcat	gctttttgtc	cctccggcac	300
cagttgtcaa	tactaaccgg	ctggtttgcc	tccatcacat	ttgtgatctg	tagctctgga	360
tacatctcct	gacagtactg	aagaacttct	tcttttgttt	caaaagcarg	tcttgggtgcc	420
tgttggatca	ggttcccatt	tcccagtcyg	aatgttcaca	tggtcatatt	wacttcccac	480
aaaacattgc	gatttgaggc	tcagcaacag	caaactctgt	tccggcattg	gctgcaagag	540
cctcgatgta	gccggccagc	gccaaaggcag	gcgccgtgag	ccccaccagc	agcagaagca	600
g						601

<210> 193

<211> 608

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(608)

<223> n = A,T,C or G

<400> 193

atacagccca	natcccacca	cgaagatgcg	cttggtgact	gagaacctga	tgcggtcact	60
ggtcccgtg	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgactctytt	120
cccaacgcag	gcagmagcgg	gsccgggtcaa	tgaactccay	tcgtggcttg	gggtkgacgg	180
tkaagtgcag	gaagaggctg	accacctcgc	ggtccaccag	gatgcccag	tgtagcgggac	240
ctgcagcgaa	actcctcgat	ggatcatgagc	gggaagcgaa	tgaggcccag	ggccttgccc	300

```

agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctccggcctcg      360
gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgcgcgctc      420
caggammgsc accagcgtgt ccaggtcaat gtcgggtgaag ccctccgcgg gtrattggcgt      480
ctgcagtgtt tttgtcgatg ttctccaggc acaggtggc cagctgcggg tcatcgaaga      540
gtcgcgcctg cgtgagcagc atgaaggcgt tgcgggctcg cagttcttct tcaggaaactc      600
cacgcaat                                     608

```

&lt;210&gt; 194

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(392)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 194

```

gaacggctgg accttgccctc gcattgtgct tgcgggcagg gaataccttg gcaagcagyt      60
ccagtcgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggcttcccc      120
tccgcctcaa tgcagaacca gtagtgggag cactgtgttt agagttaaga gtgaacactg      180
tttgatttta cttgggaatt tcctctgtta tatagctttt cccaatgcta atttccaaac      240
aacaacaaca aaataacatg tttgcctgtt aagttgtata aaagtaggtg attctgtatt      300
taaagaaaat attactgtta catatactgc ttgcaatttc tgtatttatt gktnctstgg      360
aaataaatat agttattaaa gggtgtcant cc                                     392

```

&lt;210&gt; 195

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(502)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 195

```

ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg      60
ccgagctgag gcagatgttc ccacagtgac cccagagacc stgggstata gtytctgacc      120
cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc      180
aagggaaggc ccattccgg ggstgttccc cgaggaggaa ggaaggggc tctgtgtgcc      240
cccasgagg aagaggccct gagtcctggg atcagacacc cttcacgtg tatccccaca      300
caaatgcaag ctaccaagg tccccctca gtccccctcc stacaccctg amcgccact      360
gscscacacc caccagagc acgccaccgc ccatggggar tgtgctcaag gartcgcnng      420
gcargtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt      480
gctnanaaaa aaaaanaaaa aa                                     502

```

&lt;210&gt; 196

&lt;211&gt; 665

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(665)

<223> n = A,T,C or G

<400> 196

```

ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc      60
cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt      120
wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga      180
actwatttat tatcttgta aaagtataac aatgaaaatt ttgttcatac tgtattkac      240
aagtatgatg aaaagcaawa gatataatatt cttttattat gttaaattat gattgccatt      300
attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact      360
tcacttggtt attttattgt aaatgartta caaaattcct aatttaagar aatggatgt      420
watatttatt tcattaattt ctttcctkgt ttacgtwaat tttgaaaaga wtgcattgatt      480
tcttgacaga aatcgatcct gatgctgtgg aagtagtttg acccacatcc ctatgagttt      540
ttcttagaat gtataaagggt ttagagcccat cnaacttcaa agaaaaaaat gaccacatac      600
tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan      660
aagtg                                         665

```

<210> 197

<211> 492

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(492)

<223> n = A,T,C or G

<400> 197

```

tttntttttt ttttttttgc aggaaggatt ccattttattg tggatgcatt ttcacaatat      60
atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg      120
aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtana gatnacagag      180
aattatagtc naaccagtaa acnagggaatt tacttttcaa aagattaaat ccaaactgaa      240
caaaattcta ccctgaaact tactccatcc aaatattgga ataanagtca gcagtgtac      300
attctcttct gaactttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct      360
tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc      420
catttcactc ccatcacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg      480
ancntggctt aa                                         492

```

<210> 198

<211> 478

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(478)

<223> n = A,T,C or G

<400> 198

```

tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa      60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac      120
tgagtatatt ttgaaaagga caagttttaa gtanacncat attgccganc atancacatt      180
tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaaanaat      240
natatatgtc aatcngattt aagatacaaa acagatccta tggtagatan catcntgtag      300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta      360
agcattctag tacctctact ccatgggttaa gaatcgta caatgttta catatgtnc      420

```

gggtaagaat tgtgttaagt naanttatgg agaggtccan gagaaaaatt tgatncaa 478

<210> 199

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 199

agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta	60
tgctagtcc tgcctctat tcgctactaa atgcagactg gaggggacca aaaaggggca	120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga	180
agtgattcag ttctctctac ggatgagaga ctggctcaag aatatactca tgcagcttta	240
tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga	300
aaatttacct ggaangaaaag aggccttngg ctggggacca tccattgaa ccttctctta	360
anggacttta agaanaaaact accacatgtn tgtngtatcc tgggtgccngg ccgtttantg	420
aacntngacn ncacccttnt ggaatanant cttgacngcn tccatgaactt gctcctctgc	480
ga	482

<210> 200

<211> 270

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(270)

<223> n = A,T,C or G

<400> 200

cgccgcgaag tgcaactcca gctggggccg tgcggacgaa gattctgcc a gcagttggtc	60
cgactgagac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc	120
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gacctgacg ccgtcgggga	180
cagccggaac agagcccggg gaangcggga ggcctcgggg agcccctcgg gaagggcggc	240
ccgagagata cgcaggtgca ggtggccgcc	270

<210> 201

<211> 419

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(419)

<223> n = A,T,C or G

<400> 201

tttttttttt ttttggaaac tactgagagc acagcaggtc agcaacaagt ttattttgca	60
gctagcaagg taacagggta gggcatgggt acatgttcag gtcaacttcc ttgtcgtgg	120
ttgattgggt tgtctttatg ggggcggggg ggggtagggg aaancgaagc anaantaaca	180
tggagtgggt gcaccctccc tgtagaacct gggtacnaaa gcttggggca gttcacctgg	240

```
tctgtgaccg tcattttctt gacatcaatg ttattagaag tcaggatata ttttagagag 300
tccactgtnt ctggaggag attagggttt cttgccana tccaancaa atccacntga 360
aaaagtggga tgatncangt acngaatacc ganggcatan ttctcatant cggtgacca 419
```

<210> 202

<211> 509

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(509)

<223> n = A,T,C or G

<400> 202

```
ttnttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
tggcacttaa tccattttta tttcaaaatg tctacaaant ttnaatncnc cattatacng 120
gtntttttnc aaaatctaaa nnttattcaa attnagcca aantccttac ncaaattnaa 180
tacnncnaaa aatcaaaaaat atacntntct ttcagcaaac ttngttacat aaattaaaaa 240
aatatatacg gctgggtgtt tcaaagtaca attatcttaa cactgcaaac atnttttnaa 300
ggaactaaaa taataaaaaa cactnccgca aagggttaaag ggaacaacaa attcntttta 360
caacancnnc nattataaaa atcatatctc aaatcttagg ggaatatata cttcacacng 420
ggatcttaac ttttactnca ctttgtttat ttttttanaa ccattgtntt gggcccaaca 480
caatggnaat nccnccnncn tggactagt 509
```

<210> 203

<211> 583

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(583)

<223> n = A,T,C or G

<400> 203

```
tttttttttt ttttttttga ccccccctct ataaaaaaca agttaccatt ttattttact 60
tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac 120
taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt 180
gaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc 240
atttttcttg tctttaaaat tatctaattc ttccattttt tccctattcc aagtcaattt 300
gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttcctaaa 360
agggaaca ggaagagana atggcacaca aaacaaacat tttatattca tatttctacc 420
tacgttaata aaatagcatt ttgtgaagcc agctcaaaag aaggcttaga tccttttatg 480
tccattttag tcactaaacg atatcnaaag tgccagaatg caaaagggtt gtgaacattt 540
attcaaaagc taatataaga tatttcacat actcatcttt ctg 583
```

<210> 204

<211> 589

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(589)

<223> n = A,T,C or G

<400> 204

ttttttttnt	tttttttttt	tttttttctc	ttcttttttt	ttganaatga	ggatcgagtt	60
tttctactct	tagatagggc	atgaagaaaa	ctcatctttc	cagctttaaa	ataacaatca	120
aatctcttat	gctatatcat	attttaagtt	aaactaatga	gtcactggct	tatctttctc	180
tgaaggaaat	ctgttcattc	ttctcattca	tatagttata	tcaagtacta	ccttgcatat	240
tgagaggttt	ttctttctta	tttacacata	tatttccatg	tgaatttgta	tcaaaccctt	300
attttcatgc	aaactagaaa	ataatgtntt	cttttgcata	agagaagaga	acaatatnag	360
cattacaaaa	ctgctcaaat	tgtttgttaa	gnttatccat	tataattagt	tnggcaggag	420
ctaatacaaa	tcacatttac	ngacnagcaa	taataaaact	gaagtaccag	ttaaatatcc	480
aaaataatta	aaggaacatt	tttagcctgg	gtataattag	ctaattcact	ttacaagcat	540
ttattnagaa	tgaattcaca	tgttattatt	ccntagccca	acacaatgg		589

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(545)

<223> n = A,T,C or G

<400> 205

tttttttttt	tttttttcagt	aataatcaga	acaatattta	tttttatatt	taaaattcat	60
agaaaagtgc	cttacattta	ataaaagttt	gtttctcaaa	gtgatcagag	gaattagata	120
tngtcttgaa	caccaatatt	aatttgagga	aaatacacca	aaatacatta	agtaaattat	180
ttaagatcat	agagcttgta	agtgaaga	taaaatttga	cctcagaaac	tctgagcatt	240
aaaaatccac	tattagcaaa	taaattacta	tggacttctt	gctttaattt	tgtgatgaat	300
atgggggtgc	actggtaaac	caacacattc	tgaaggatac	attacttagt	gatagattct	360
tatgtacttt	gctanatnac	gtggatatga	gttgacaagt	ttctctttct	tcaatctttt	420
aaggggcnga	ngaaatgagg	aagaaaagaa	aaggattacg	catactgttc	tttctatngg	480
aaggattaga	tatgtttcct	ttgccaatat	taaaaaata	ataatgttta	ctactagtga	540
aacc						545

<210> 206

<211> 487

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(487)

<223> n = A,T,C or G

<400> 206

tttttttttt	tttttttagtc	aagtttctna	tttttattat	aattaaagtc	ttggtcattt	60
catttattag	ctctgcaact	tacatattta	aattaaagaa	acgttnttag	acaactgtna	120
caatttataa	atgtaagggtg	ccattattga	gtanatatat	tcctccaaga	gtggatgtgt	180
cccttctccc	accaactaat	gaancagcaa	cattagttta	attttattag	tagatnatac	240
actgctgcaa	acgctaattc	tcttctccat	ccccatgtn	atattgtgta	tatgtgtgag	300
ttggtnagaa	tgcatcanca	atctnacaat	caacagcaag	atgaagctag	gcntgggctt	360
tcggtgaaaa	tagactgtgt	ctgtctgaat	caaagtatct	gacctatcct	cggtggcaag	420
aactcttcga	accgcttcct	caaaggcngc	tgccacattt	gtggcntctn	ttgcacttgt	480

ttcaaaa

487

&lt;210&gt; 207

&lt;211&gt; 332

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(332)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 207

tgaattggct	aaaagactgc	atTTTTanaa	ctagcaactc	ttatttcttt	ccttttaaaa	60
tacatagcat	taaatcccaa	atcctattta	aagacctgac	agcttgagaa	ggtcactact	120
gcatttatag	gaccttctgg	tggttctgct	gttacntttg	aantctgaca	atccttgana	180
atctttgcat	gcagaggagg	taaaaggtat	tggattttca	cagaggaana	acacagcgca	240
gaaatgaagg	ggccaggctt	actgagcttg	tccactggag	ggctcatggg	tgggacatgg	300
aaaagaaggc	agcctaggcc	ctggggagcc	ca			332

&lt;210&gt; 208

&lt;211&gt; 524

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(524)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 208

agggcgtggt	gcgaggggcg	ttactgtttt	gtctcagtaa	caataaatac	aaaaagactg	60
gttgtgttcc	ggccccatcc	aaccacgaag	ttgatttctc	ttgtgtgcag	agtgactgat	120
tttaaaggac	atggagcttg	tcacaatgtc	acaatgtcac	agtgtgaagg	gcacactcac	180
tcccgcgtga	ttcacattta	gcaaccaaca	atagctcatg	agtccatact	tgtaaatact	240
tttggcagaa	tacttnttga	aacttgcaag	tgataactaa	gatccaagat	atttcccaaa	300
gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagcccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgatcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcaatc	atctatccaa	480
aaaccattac	ctgatccact	tccggtaatg	caccaccttg	gtga		524

&lt;210&gt; 209

&lt;211&gt; 159

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 209

gggtgaggaa	atccagagtt	gccatggaga	aaattccagt	gtcagcattc	ttgctccttg	60
tggccctctc	ctacactctg	gccagagata	ccacagtcaa	acctggagcc	aaaaaggaca	120
caaaggactc	tcgacccaaa	ctgccccaga	ccctctcca			159

&lt;210&gt; 210

&lt;211&gt; 256

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (256)  
<223> n = A,T,C or G

<400> 210  
actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc 60  
actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta 120  
tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180  
ttgcagggtg naaatgggan ggctggtttg ttanatgaac agggacatag gaggtaggca 240  
ccaggatgct aaatca 256

<210> 211  
<211> 264  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (264)  
<223> n = A,T,C or G

<400> 211  
acattgtttt tttgagataa agcattgaga gagctctcct taacgtgaca caatggaagg 60  
actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120  
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gttaaggaga 180  
ggggagatac attcngaaag aggactgaaa gaaataactca agtnggaaaa cagaaaaaga 240  
aaaaaaggag caaatgagaa gcct 264

<210> 212  
<211> 328  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (328)  
<223> n = A,T,C or G

<400> 212  
acccaaaaat ccaatgctga atatttggtc tcattattcc canattcttt gattgtcaaa 60  
ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120  
gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccggcag 180  
ttnaatttca ttccattga cttgggatcc ttatcatcag ccagagagat tgaaaaattta 240  
cccctacnac tctttactct ctgganaggg ccagtgggtg tagctataag cttggccaca 300  
tttttttttc ctttattcct ttgtcaga 328

<210> 213  
<211> 250  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature



<222> (1)...(250)

<223> n = A,T,C or G

<400> 213

acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt	60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgcca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatata tctctnacct	240
tctcatcggt	250

<210> 214

<211> 444

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(444)

<223> n = A,T,C or G

<400> 214

accagaatc caatgctgaa tatttggtt cattattccc agattctttg attgtcaaag	60
gatttaatgt tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg	120
tttatatatg cagcaacaat attcaagcgc gacaacaggt tattgaactt gcccggcagg	180
tgaatttcat tccattgac ttgggatcct tatcatcagc canagagatt gaaaatttac	240
cctacgact ctttactctc tggagagggc cagtgtgtgt agctataagc ttggccacat	300
ttttttttcc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag	360
agtgaacttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt	420
actttgctct ccctaataata cctc	444

<210> 215

<211> 366

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(366)

<223> n = A,T,C or G

<400> 215

acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt	60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgcca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatata tctctgacct	240
tctcatcggt aagcagaggc ttaggcaac atggaccata gcgaanaaaa aacttagtaa	300
tccaagctgt tttctacact gtaaccaggt ttccaaccaa ggtggaaatc tcctatactt	360
ggtgcc	366

<210> 216

<211> 260

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature  
<222> (1)...(260)  
<223> n = A,T,C or G

<400> 216  
ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60  
caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctntnc atttttttat 120  
taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttaaaa 180  
atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240  
aattcttctt tccctccttt 260

<210> 217  
<211> 262  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(262)  
<223> n = A,T,C or G

<400> 217  
acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60  
tcttgccat aattttctat ttttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120  
ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180  
atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttaccta 240  
atatacttca tgcttgtaaa gt 262

<210> 218  
<211> 205  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(205)  
<223> n = A,T,C or G

<400> 218  
accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60  
cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120  
aggcctcccc agttctactg acctttgtcc ttangtntna ngccagggt tgctaggaaa 180  
anaaatcagc agacacaggt gtaaa 205

<210> 219  
<211> 114  
<212> DNA  
<213> Homo sapien

<400> 219  
tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60  
accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220  
<211> 93

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 220

actagccagc acaaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta	60
aaataagcat ttagtgctca gtcctactg agt	93

&lt;210&gt; 221

&lt;211&gt; 167

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(167)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 221

actangtgca ggtgcgcaca aatatttgtc gatattccct tcattcttga ttccatgagg	60
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc	120
ccccactac ctccctgac gctccccana aatcacccaa cctctgt	167

&lt;210&gt; 222

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 222

agggcgtggg gcggaggggc gtactgacct cattagtagg aggatgcatt ctggcacccc	60
gttcttcacc tgtccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa	120
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa	180
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt	240
taggtgagca tgattagaga gctttaggtg tgcttttaca tatatctggc atatttgagt	300
ctcgtatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t	351

&lt;210&gt; 223

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(383)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 223

aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat	60
tggttaattat ggtcaattta atwrtttkt ggggcatttc cttacattgt cttgacaaga	120
ttaaaatgtc tgtgccaaaa ttttgatatt tatttgagga cttcttatca aaagtaatgc	180
tgccaaagga agtctaagga attagtagtg ttcccmteac ttgtttggag tgtgctattc	240
taaaagattt tgatttcctg gaatgacaat tatattttta ctttggtggg ggaaanagtt	300
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg	360
accattaagc tatatgttta aaa	383

&lt;210&gt; 224

<211> 320  
 <212> DNA  
 <213> Homo sapien

<400> 224  
 ccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60  
 aaaagtttgt gacattgtag tagggagtg gtaccctta ctcccatca aaaaaaaat 120  
 ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa 180  
 gagaaaatac tactttctcr aaatggaagc ccttaaaggt gctttgatac tgaaggacac 240  
 aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgagc 300  
 tttaractcm gcattgtgac 320

<210> 225  
 <211> 1214  
 <212> DNA  
 <213> Homo sapien

<400> 225  
 gaggactgca gcccgcactc gcagccctgg caggcggcac tggtcattga aaacgaattg 60  
 ttctgctcgg gcgtcctggg gcattccgag tgggtgctgt cagccgcaca ctgtttccag 120  
 aactcctaca ccatcgggct gggcctgcac agtcttgagg ccgaccaaga gccagggagc 180  
 cagatgggtgg aggccagcct ctccgtacgg caccagagt acaacagacc cttgctcgct 240  
 aacgacctca tgcctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300  
 atcagcattg cttcgagtg ccctaccgcg gggaaactctt gcctcgtttc tggctggggg 360  
 ctgctggcga acggcagaat gcctaccgtg ctgacgtgcg tgaacgtgtc ggtgggtgtc 420  
 gaggaggtct gcagtaagct ctatgacccg ctgtaccacc ccagcatgtt ctgcgcggc 480  
 ggagggcaag accagaagga ctctgcaac ggtgactctg gggggccctt gatctgcaac 540  
 gggtaacttg agggccttgt gtctttcgga aaagcccgt gtggccaagt tggcgtgcca 600  
 ggtgtctaca ccaacctctg caaattcact gactggatag agaaaaccgt ccaggccagt 660  
 taactctggg gactgggaac ccatgaaatt gacccccaaa tacatcctgc ggaaggaatt 720  
 caggaatatc tgttcccagc ccctcctccc tcaggcccag gactccaggc cccagccccc 780  
 tcctcctca aaccaagggg acagatcccc agcccctcct ccctcagacc caggagtcca 840  
 gacccccag cccctcctcc ctccagacca ggagtccagc ccctcctccc tcagaccag 900  
 gagtccagac cccccagccc ctctcctccc agaccaggg gtccaggccc ccaaccctc 960  
 ctccctcaga ctccagaggtc caagccccca acccctcctt cccagacccc agaggtccag 1020  
 gtcccagccc ctctcctccc agaccagcg gtccaatgcc acctagactc tccctgtaca 1080  
 cagtgcctcc ttgtggcacg ttgacccaac cttaccagtt ggtttttcat tttttgtccc 1140  
 tttcccttag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaaaaaaaa aaaa 1214

<210> 226  
 <211> 119  
 <212> DNA  
 <213> Homo sapien

<400> 226  
 acccagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa 60  
 agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<400> 227

acaattcata	gggacgacca	atgaggacag	ggaatgaacc	cggctctccc	ccagccctga	60
tttttgctac	atatggggtc	ccttttctatt	ctttgcaaaa	acactgggtt	ttctgagaac	120
acggacgggt	cttagcacaa	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttcttc	ctctggagga	aaggtggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgtcccc	ttccaatcag	ccacttctga	gaacccccat	ctaacttctt	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaagggtg	caccctcagc	agagaagccg	agagcttaac	tctggtcgtt	tccagagaca	480
acctgctggc	tgtcttgga	tgcgcccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcattgagag	600
gacaggctct	gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggtt	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818

&lt;210&gt; 228

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 228

actggagaca	ctgttgaact	tgatcaagac	ccagaccacc	ccaggtctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaaacga	gcctcctcct	tggagatgg	aagaccgtgt	120
tcgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gcggagtcac	atttcaatgg	180
taggaaaagt	ggcttcgtaa	aatagaagag	cagtcactgt	ggaactacca	aatggcgaga	240
tgctcgggtc	acattggggg	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggccagttt	gttccactga	agcttttccc	acagcagtc	acctctgcag	360
gctggcagct	gaatggcctg	ccggtggctc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	gttggctcct	tccaggtttg	480
ccagacgggtg	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctgggtga	cagtgacccg	540
ccgtggtatg	ccttggccca	ttccagcagt	cccagttatg	catttcaagt	ttggggtttg	600
ttcttttctg	taatgttctt	ctgtgtgttc	agctgtcttc	atttcctggg	ctaagcagca	660
ttgggagatg	tggaccagag	atccactcct	taagaaccag	tggcgaaaga	cacttttctt	720
cttactctg	aagtagctgg	tggt				744

&lt;210&gt; 229

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatccaaa	tcattgtgaac	60
cattacacat	cgaaataaaa	gaaagggtgg	agacttgccc	aacgccaggc	tgacatgtgc	120
tgcagggttg	ttgtttttta	attattattg	ttagaaacgt	caccacacgt	ccctgttaat	180
ttgtatgtga	cagccaactc	tgagaagggtc	ctatttttcc	acctgcagag	gatccagtct	240
cactaggctc	ctccttgccc	tcacactgga	gtctccgcca	gtgtgggtgc	ccactgacat	300

&lt;210&gt; 230

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 230

cagcagaaca	aatacaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120

caatataaag	tcttggttca	cactcaggaa	cgagagctga	cccagttaag	ggagaagttg	180
cggggaagga	gagatgcctc	cctctcattg	aatgagcatc	tccaggccct	cctcactccg	240
gatgaaccgg	acaagtccca	ggggcaggac	ctccaagaaa	cagacctcgg	ccgcgaccac	300
g						301

&lt;210&gt; 231

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 231

gcaagcacgc	tggcaaatct	ctgtcagggtc	agctccagag	aagccattag	tcatttttagc	60
caggaactcc	aagtccacat	ccttggcaac	tggggacttg	cgaggttag	ccttgaggat	120
ggcaacacgg	gacttctcat	caggaagtgg	gatgtagatg	agctgatcaa	gacggccagg	180
tctgaggatg	gcaggatcaa	tgatgtcagg	ccggttggtg	ccgccaatga	tgaacacatt	240
tttttttgtg	gacatgccat	ccattttctgt	caggatctgg	ttgatgactc	ggtcagcagc	300
c						301

&lt;210&gt; 232

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 232

agtaggtatt	tcgtgagaag	ttcaacacca	aaactggaac	atagttctcc	ttcaagtgtt	60
ggcgacagcg	gggcttcctg	attctggaat	ataactttgt	gtaaattaac	agccacctat	120
agaagagtcc	atctgctgtg	aaggagagac	agagaactct	gggttccgtc	gtcctgtcca	180
cgtgctgtac	caagtgtctg	tgccagcctg	ttacctgttc	rcactgaaaa	tctggctaata	240
gctcttgtgt	atcacttctg	attctgacaa	tcaatcaatc	aatggcctag	agcactgact	300
g						301

&lt;210&gt; 233

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 233

atgactgact	ttccagtaag	gctctctaa	gggtaagtag	gaggatccac	aggatttgag	60
atgctaaggc	cccagagatc	gtttgatcca	accctcttat	tttcagaggg	gaaaatgggg	120
cctagaagtt	acagagcatc	tagctgggtc	gctggcacc	ctggcctcac	acagactccc	180
gagtagctgg	gactacaggc	acacagtcac	tgaagcaggc	cctgttagca	attctatgcg	240
tacaaattaa	catgagatga	gtagagactt	tattgagaaa	gcaagagaaa	atcctatcaa	300
c						301

&lt;210&gt; 234

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 234

aggtcctaca	catcgagact	catccatgat	tgatatgaat	ttaaaaatta	caagcaaaga	60
cattttatcc	atcatgatgc	tttcttttct	ttcttctttt	cgttttcttc	tttttctttt	120
tcaatttcag	caacatactt	ctcaaattct	tcaggattta	aaatcttgag	ggattgatct	180
cgctcatga	cagcaagttc	aatgtttttg	ccacctgact	gaaccacttc	caggagtgcc	240
ttgatcacca	gcttaatggg	cagatcatct	gcttcaatgg	cttcgtcagt	atagttcttc	300

t

301

<210> 235  
 <211> 283  
 <212> DNA  
 <213> Homo sapien

<400> 235

tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg	60
aattccctca tcttttaggg aatcatttac caggtttgga gaggattcag acagctcagg	120
tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata	180
atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatcaaca	240
ttagggattc aaagaaatat tagattttaag ctcacactgg tca	283

<210> 236  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 236

aggtcctcca ccaactgcct gaagcacggg taaaattggg aagaagtata gtgcagcata	60
aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg	120
tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatag	180
tgggtagacg gcttcatgag tacagtgtac tgtggtatcg taatctggac ttgggttgta	240
aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc	300
a	301

<210> 237  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 237

cagtggtagt ggtgggtggac gtggcggttg tcgtgggtgcc ttttttggtg cccgtcacaa	60
actcaatttt tgttcgctcc tttttggcct tttccaattt gtccatctca attttctggg	120
ccttggctaa tgcctcatag taggagtcct cagaccagcc atggggatca aacatattct	180
ttgggtagtt ggtgccaaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaattcta	240
gggttccgaa attctttctt cctttggata atgtagttca tatccattcc ctcttttatt	300
t	301

<210> 238  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 238

gggcaggttt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt	60
gttcacagtt cagccccctg ctcaagaaac caacgggcca gctaaggaga ggaggaggca	120
ccttgagact tccggagtcg aggccttcca gggttcccca gcccatcaat cattttctgc	180
acccccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca	240
gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aattttctta	300
t	301

<210> 239  
 <211> 239

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 239

ataagcagct aggggaattct ttatttagta atgtcctaac ataaaagttc acataactgc	60
ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa	120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgccg gcatacacag tatacaggtc cttcaggga	239

&lt;210&gt; 240

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 240

ggtcctaatag aagcagcagc ttccacattt taacgcagggt ttacgggtgat actgtccttt	60
gggatctgcc ctccagtggg accttttaag gaagaagtgg gcccaagcta agttccacat	120
gctgggtgag ccagatgact tctgttcctt ggctactttc ttcaatgggg cgaatggggg	180
ctgccagggt tttaaaatca tgcttcatct tgaagcacac ggctacttca cctcctcac	240
gctgtgggtg tactttgatg aaaatacca cttgtttggc ctttctgaag ctataatgtc	300

&lt;210&gt; 241

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 241

gaggtctggt gctgaggtct ctgggctagg aagaggaggt ctgtggagct ggaagccaga	60
cctcttttga ggaaactcca gcagctatgt tgggtgtctct gagggaatgc aacaaggctg	120
ctcctccatg tattggaaaa ctgcaaactg gactcaactg gaaggaagtg ctgctgccag	180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct	240
tcctcctcct gtcatacggg ctctctcaag catcctttgt tgtcaggggc ctaaaaggga	300
g	301

&lt;210&gt; 242

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 242

ccgaggtcct gggatgcaac caatcactct gtttcacgtg acttttatca ccatacaatt	60
tgtggcattt cctcattttc tacattgtag aatcaagagt gtaataaat gtatatcgat	120
gtcttcaaga atatatcatt cctttttcac tagaaccat tcaaatata agtcaagaat	180
cttaatatca acaatatat caagcaaact ggaaggcaga ataactacca taatttagta	240
taagtacca aagttttata aatcaaaagc cctaagtata accattttta gaattcaatc	300
a	301

&lt;210&gt; 243

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 243

aggtaagtcc cagtttgaag ctcaaaagat ctggatagag cataggctca tcgacgacat	60
ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg	120



tgacgtgcag tcggactctg tggcccaagg gtatggctct ctccggcatga tgaccagcgt 180  
 gctggtttgt ccagatggca agacagtaga agcagaggct gccacaggga ctgtaacccg 240  
 tcactaccgc atgttccaga aaggacagga gacgtccacc aatcccattg cttccatttt 300  
 t 301

<210> 244  
 <211> 300  
 <212> DNA  
 <213> Homo sapien

<400> 244  
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 gtcattgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc 120  
 ccagggaacct tggaaacagt tgacactgta aggtgcttgc tccccaaagac acatccctaaa 180  
 aggtgttgta atgggtgaaaa cgtcttcctt ctttattgcc ctttcttatt tatgtgaaca 240  
 actgtttgtc ttttgtgtat cttttttaa ctgtaaagtt caattgtgaa aatgaatc 300

<210> 245  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 245  
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 tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt 120  
 aaggccagga gatattgtca ttaatgtara cttcaggaca ctagagtata gcagccctat 180  
 gttttcaaag agcagagatg caattaaata ttgttttagca tcaaaaaggc cactcaatac 240  
 agctaataaa atgaaagacc taatttctaa agcaattcct tataatttac aaagttttaa 300  
 g 301

<210> 246  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 246  
 ggtctgtcct acaatgcctg cttcttgaaa gaagtcggca ctttctagaa tagctaaata 60  
 acctgggctt attttaaaga actatttgta gctcagattg gttttcctat ggctaaaata 120  
 agtgcttctt gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac 180  
 taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc 240  
 caaatgtgtc ttacaaaaca cgctcctaac aagggtatgct ttacactacc aatgcagaaa 300  
 c 301

<210> 247  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 247  
 aggtcctttg gcagggtca tggatcagag ctcaaactgg agggaaaggc atttcgggta 60  
 gcctaagagg gcgactggcg gcagcacaac caaggaaggc aagggtgttt cccccacgct 120  
 gtgtcctgtg ttcagggtcg acacacaatc ctcatgggaa caggatcacc catgctgtgc 180  
 ccttgatgat caaggttggg gcttaagtgg attaagggag gcaagttctg ggttccttgc 240  
 cttttcaaac catgaagtca ggctctgtat ccctcctttt cctaactgat attctaacta 300  
 a 301

<210> 248  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 248  
 aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60  
 attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttaagaatt 120  
 acaggaagaa agtgggttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180  
 gtacattcca gcctgttggc aactccataa aaacatttca gattttaatc ccgaatttag 240  
 ctaatgagac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300  
 c 301

<210> 249  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 249  
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 ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgcgc 120  
 ccagggagac acagcagtga ctcagagctg gtgcgacact gtgcctccct cctcaccgcc 180  
 catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag 240  
 actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt 300  
 a 301

<210> 250  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 250  
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 cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120  
 cataagcaca tcagtacttt tctctggctg gaatagtaaa cttaaagtatg gtacatctac 180  
 ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240  
 caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300  
 a 301

<210> 251  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 251  
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 agacaacctc atagagcata ggagaactgg ttgccctggg gccaggggga ctgtctggat 120  
 gccaggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180  
 cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgga 240  
 cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatatcct 300  
 c 301

<210> 252  
 <211> 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 252

gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttcctca	60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtcctt caagaatata	120
tcatttccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa	180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taccctaaagt	240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc	300
a	301

&lt;210&gt; 253

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 253

ttccctaaga agatgttatt ttgttggggtt ttgttccccc tccatctcga ttctcgtacc	60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctcccttagct	120
tggtctgatt gttttcagac cttaaaatat aaacttggtt cacaagcttt aatccatgtg	180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt	240
tccatagtgc ccacagggtta ttcctcacat tttctccata ggaaaatgct tttcccaag	300
g	301

&lt;210&gt; 254

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 254

cgctgcgcct ttcccttggg ggagggggcaa ggccagaggg ggtccaagtg cagcacgagg	60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc	120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa	180
gaaaaaataa aagcttttga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc	240
acttaaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc	300
t	301

&lt;210&gt; 255

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 255

agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtctc tttattataa	60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat	120
tgggattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg	180
aggaaaaagg actggagggtg gaatctttat aaaaaacaag agtgattgag gcagattgta	240
aacattatta aaaaaaaga aacaaacaaa aaaaatagaga aaaaaaccac cccaacacac	300
aa	302

&lt;210&gt; 256

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 256  
gttccagaaa acattgaagg tggcttccca aagtctaact agggataccc cctctagcct 60  
aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc 120  
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat 180  
aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt 240  
gtggcctctc ggcctgggta gcaagaacat tcagggtagg cctaagttan tcgtgttagt 300  
t 301

<210> 257  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 257  
gttgtggagg aactctggct tgctcattaa gtcctactga ttttcactat cccctgaatt 60  
tccccactta tttttgtctt tcaactatcg aggccttaga agaggtctac ctgcctccag 120  
tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat 180  
gtcacattac tcccttcagt gatttcttgt agaagtgcc atccctgaat gccaccaaga 240  
tcttaatctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc 300  
c 301

<210> 258  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 258  
cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc 60  
aggggcccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120  
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttacactg 180  
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtgggtgtcat 240  
tgggtgatccc tgggagcgcc ggtggagtaa cgttgggtcca tggaaagcag cgcccacaac 300  
t 301

<210> 259  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 259

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tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg      60
gtgtcctgaa gtgatttggg cccctgaggg cagacaccta agtaggaatc ccagtgggaa      120
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtggggccag gaaggtctgt      180
tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggctt      240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcatecttgg ctccaggtgg      300
c

```

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<210> 260
<211> 301
<212> DNA
<213> Homo sapien

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<400> 260
tttttttctt ccctaaggaa aaagaaggaa caagtctcat aaaaccaa at aagcaatggt      60
aaggtgtctt aacttgaaaa agattaggag tctctggttt acaagttata attgaatgaa      120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaacia caggattaac      180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttaataaac agactgattc      240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca      300
c

```

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<210> 261
<211> 301
<212> DNA
<213> Homo sapien

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<400> 261
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tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggtt      120
agcaccaact attccataca attcatcagc aggaaataaa ggctcttcag aaggttcaat      180
ggtagacatc aatttcttct gataatttag attcctcaca accttcttag ttaagtgaag      240
ggcatgatga tcatccaaag ccagtggtc acttactcca gactttctgc aatgaagatc      300
a

```

```

<210> 262
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 262
gaggagagcc tggtacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc      60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaatac ctgagtcacc      120
cctagacttc ctaaaccaga tctctggggg ctggaacctg gcaactctga tttgtaatga      180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgccc      240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat      300
c

```

```

<210> 263
<211> 301
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

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&lt;400&gt; 263

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ttcttagtat	tatttatggg	aaataggctc	ttaccacttg	caaataactg	gccacatcat	180
taatgactga	cttcccagta	aggctctcta	aggggtaagt	angaggatcc	acaggatttg	240
agatgctaag	gccccagaga	tcgtttgatc	caaccctctt	attttcagag	gggaaaatgg	300
g						301

&lt;210&gt; 264

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 264

aaagacgtta	aaccactcta	ctaccacttg	tggaactctc	aaagggtaaa	tgacaaascc	60
aatgaatgac	tctaaaaaca	atattttacat	ttaatggttt	gtagacaata	aaaaaacaag	120
gtggatagat	ctagaattgt	aacattttta	gaaaaccata	scatttgaca	gatgagaaag	180
ctcaattata	gatgcaaagt	tataactaaa	ctactatagt	agtaaagaaa	tacatttcac	240
acccttcata	taaattcact	atcttggcct	gaggcactcc	ataaaatgta	tcacgtgcat	300
a						301

&lt;210&gt; 265

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 265

tgcccaagtt	atgtgtaagt	gtatccgcac	ccagaggtaa	aactacactg	tcattctttgt	60
cttcttgtga	cgcagtatct	cttctctggg	gagaagccgg	gaagtcttct	cttggctcta	120
catattcttg	gaagtctcta	atcaactttt	gttccatttg	tttcatttct	tcaggagggga	180
ttttcagttt	gtcaacatgt	tctctaacaa	cacttgccca	tttctgtaaa	gaatccaaag	240
cagtccaagg	ctttgacatg	tcaacaacca	gcataactag	agtatccttc	agagatacgg	300
c						301

&lt;210&gt; 266

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 266

taccgtctgc	ccttctctcc	atccaggcca	tctgcgaatc	tacatgggtc	ctcctattcg	60
acaccagatc	actctttcct	ctaccacacag	gcttgctatg	agcaagagac	acaacctcct	120
ctcttctgtg	ttccagcttc	ttttcctgtt	cttcccaccc	cttaagttct	attcctgggg	180
atagagacac	caataccat	aacctctctc	ctaagcctcc	ttataacca	gggtgcacag	240
cacagactcc	tgacaactgg	taaggccaat	gaactgggag	ctcacagctg	gctgtgcctg	300
a						301

&lt;210&gt; 267

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 267

aaagagcaca	ggccagctca	gcctgccctg	gccatctaga	ctcagcctgg	ctccatgggg	60
------------	------------	------------	------------	------------	------------	----

gttctcagtg ctgagtcctat ccaggaaaag ctcacctaga ccttctgagg ctgaatcttc 120  
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgggtct ggagtaaagc 180  
ctcattctga ttctctcctt tcttttcttt caagttggct ttcttcacat ccctctgttc 240  
aattcgcttc agcttgtctg ctttagccct catttccaga agcttcttct ctttggcatc 300  
t 301

&lt;210&gt; 268

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 268

aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta 60  
gatcttggga gagctgggtc ttctaaggag aaggaggaag gacagatgta accttggatc 120  
tcgaagagga agtctaattg aagtaattag tcaacgggtc ttgttttagac tcttgggaata 180  
tgctgggtgg ctcaagtggc ccttttggag aaagcaagta ttattcttaa ggagtaacca 240  
cttcccattg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact 300  
a 301

&lt;210&gt; 269

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 269

taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat 60  
aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact 120  
atagtcacag accttaataa ttcacattgt tttctatgtc tactgaaaat aagttcacta 180  
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta 240  
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc 300  
t 301

&lt;210&gt; 270

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 270

cattgaagag cttttgcgaa acatcagaac acaagtgcct ataaaattaa ttaagcctta 60  
cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120  
gagcttgctg gtgcagtgc aatttgataa cactattcat ggccgaattg atcaagtcaa 180  
ccaactcctt gaactggatc atcagaagaa ggggtggtgca cgatatactg cactagataa 240  
tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggcct aacagaaaaa 300  
a 301

&lt;210&gt; 271

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 271

aaaaggttct cataagatta acaattttaa taaatatttg atagaacatt ctttctcatt	60
tttatagctc atcttttagg ttgatattca gtccatgctt cccttgctgt tcttgatcca	120
gaattgcaat cacttcatca gcctgtattc gctccaattc tctataaagt gggccaagg	180
tgaaccacag agccacagca cacctctttc ccttggtgac tgccttcacc ccatganggt	240
tctctcctcc agatganaac tgatcatgcg cccacatttt gggttttata gaagcagtca	300
c	301

&lt;210&gt; 272

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 272

taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaagtgc	60
ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga	120
tccaataatt ccctcatgat gagcaagaaa aattctttgc gcacccctcc tgcattccaca	180
gcattcttct caacaaatat aaccttgagt ggcttcttgc aatctatgtt ctttgttttc	240
ctaaggactt ccattgcac tcctacaata ttttctctac gcaccactag aattaagcag	300
g	301

&lt;210&gt; 273

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 273

acatgtgtgt atgtgtatct ttgggaaaaa aanaagacat cttgtttayt atttttttgg	60
agagangctg ggacatggat aatcacwtaa ttgtctayta tyactttaat ctgactygaa	120
gaaccgtcta aaaataaaat ttaccatgtc dtatatctct tatagtatgc ttatttcacc	180
ttytttctgt ccagagagag tatcagtgtc ananatttma ggggtgaamac atgmattggg	240
gggacttnty tttaacngagm accctgccc ggcgcctcg makengantt ccgcsananc	300
t	301

&lt;210&gt; 274

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 274

cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg	60
aacagtaaat gattattaga gagaangaat ggaccaagag gacagaaatt aacttgtaaa	120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttgtg gaaaagtcca	180
tctaggatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc	240
aattgtgctt cttttgataa gaagctttct tggatcatatc aggaaattcc aganaaaagtc	300



c

301

&lt;210&gt; 275

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 275

tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60  
gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttgccacc aacagtaagc 120  
tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag 180  
tcaagagact cccaggcctc agcgtacctg cccgggaggc cgctcgaagc cgaattctgc 240  
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgcctat 300  
a 301

&lt;210&gt; 276

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 276

tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat 60  
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat 120  
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180  
caatacatTT aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttTgtg 240  
aaaactattc agtatgtttc ctttgcttca tgtctgagaa ggctctcctt caatggggat 300  
g 301

&lt;210&gt; 277

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 277

tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60  
atacagagga cttggaggaa gcagagcaac tgaatttaat taaaagaag gaaaacattg 120  
gaatcatggc actcctgata ctttcccaaa tcaacactct caatgccccca cctcgtcct 180  
caccatagtg gggagactaa agtggccacg gatttgccct angtgtgcag tgcgttctga 240  
gttcnctgtc gattacatct gaccagtctc ctttttccga agtcnctccg ttcaatcttg 300  
c 301

&lt;210&gt; 278

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 278  
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 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120  
 cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180  
 aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgtc tcacagggtt 240  
 tatgtgttct tcgttaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300  
 c 301

<210> 279  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 279  
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 gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120  
 ttagaccttt accttccagc caccacacag tgcttgatat ttcagagtca gtcattgggt 180  
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240  
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300  
 a 301

<210> 280  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 280  
 ggtactggag ttttcctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60  
 tagaaagggt gtggaaccaa attgtggtca atggaatatg gagaatatgg ttctcactct 120  
 tgagaaaaaa acctaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180  
 gtttgatata gtttaggggt ggggttagat taagatctaa attacatcag gacaaagaga 240  
 cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300  
 t 301

<210> 281  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 281  
 aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatatcc 60  
 gccgagcaat ccaaatcctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120  
 atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180  
 tgtgtagcac actgcgatta cagctaaata acccgatatt gtgtgtcatg tttgcatttc 240

tgacaagtga aacaggatct tacgatggag ttttgtatga aaacaaagtt gcagtacctc 300  
g 301

<210> 282  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 282  
cagggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60  
tccagaaccc aaaaattaag aaattcaaaa agacattttg tgggcacctg ttagcacaga 120  
agcgcagaag caaagcccag gcagaacctat gctaaccctta cagctcagcc tgcacagaag 180  
cgcagaagca aagcccaggc agaaccatgc taacctttaca gctcagcctg cacagaagcg 240  
cagaagcaaa gccccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300  
a 301

<210> 283  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 283  
atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag 60  
cactttgagg gctttataat aatattgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120  
gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180  
acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcattcttta 240  
ggaaacatat acatttttaa aaatctatct tatgtaagaa ctgacagacg aatttgcttt 300  
g 301

<210> 284  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 284  
cagggtacaaa acgctattaa gtggcttaga atttgaacat ttgtggtctt tatttacttt 60  
gcttcgtgtg tgggcaaagc aacatcttcc ctaaataat attaccaaga aaagcaagaa 120  
gcagattagg tttttgacaa aacaaacagg ccaaaaaggg gctgacctgg agcagagcat 180  
ggtgagaggc aaggcatgag agggcaagtt tggtgtggac agatctgtgc ctactttatt 240  
actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt 300  
a 301

<210> 285  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)... (301)  
<223> n = A,T,C or G

<400> 285  
acatcaccat gatcggtacc cccacccatt atacgttgta tgtttacata aatactcttc 60  
aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac 120

caggaaagca aatgctatctt acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180  
attaaatattg tctgacttct tttgaggtca cagcactagg caaatgctat ttacgatctg 240  
caaaagctgt ttgaagagtc aaagccccc tgtgaacacg atttctggac cctgtaacag 300  
t 301

<210> 286  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 286  
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tgtatattat ttttgcctta cagtggatca ttctagtagg aaaggacagt aagatttttt 120  
atcaaaatgt gtcatgccag taagagatgt tatattcttt tctcatttct tccccaccca 180  
aaaaaagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt 240  
gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttccttg 300  
t 301

<210> 287  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 287  
tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60  
cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatag 120  
aaatgatttg gttatgaacg cacagttagg gcagcagggc cagaatcctg accctctgcc 180  
ccgtgggttat ctctcccca gcttggctgc ctcatgttat cacagtattc cattttgttt 240  
gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggaatgc 300  
t 301

<210> 288  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 288  
gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60  
agtcaatagg aagacaaatt ccagttccag ctcatgtctg gtatctgcaa agctgcaaaa 120  
gatcttttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatat 180  
aaaagcatct gcttttgtga tttaatttag ctcatctggc cactggaaga atccaaacag 240  
tctgccttaa ttttggatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300  
a 301

<210> 289  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (301)  
<223> n = A,T,C or G

<400> 289

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<210> 290
<211> 301
<212> DNA
<213> Homo sapien
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<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G
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<210> 291
<211> 301
<212> DNA
<213> Homo sapien
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<210> 292
<211> 301
<212> DNA
<213> Homo sapien
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<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G
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<400> 292						
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aaaaccaaag	natataaccg	aaaggaaaaa	cagatgagac	ataaaatgat	ttgcnagatg	180
ggaaatatag	tasttyatga	atgtttnatta	aattccagtt	ataatagtgg	ctacacactc	240
tcactacaca	cacagacccc	acagtcctat	atgccacaaa	cacattttcca	taacttgaaa	300
a						301

<210> 293  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 293  
ggtagcaagt gctgggtgcc gctgtgtacc tgtttctcact gaaaagtctg gctaagtctc 60  
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aacacaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt 180  
gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg 240  
ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat 300  
g 301

<210> 294  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 294  
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tttaactata gtcacaganc ttaaattatc acattgtttt ctatgtctac tgaaaaataag 180  
ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240  
cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt 300  
t 301

<210> 295  
<211> 305  
<212> DNA  
<213> Homo sapien

<400> 295  
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ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccattctctga 180  
actggtagaa aaacrtctga agagctagtc tatcagcatc tgacagggtga attggatggt 240  
ttcagaacc atttcaccca gacagcctgt ttctatcctg ttaataaat tagtttgggt 300  
tctct 305

<210> 296  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 296  
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attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180  
tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt 240

tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg 300  
c 301

<210> 297

<211> 300

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 297

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aaggttttga aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga 120  
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt 180  
tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc 240  
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc acactggcgg 300

<210> 298

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 298

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tgaagctctc agatcaatca cgggaaggcg ctggcggttg tggccacctg gaaccaccct 180  
gtcctgtctg ttacatttc actaycaggt tttctctggg cattacnatt tgttccccta 240  
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t 301

<210> 299

<211> 301

<212> DNA

<213> Homo sapien

<400> 299

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tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg 180  
gagtttcgcc atgttggcca gctgggtctca aactcctgac ctcaagcgac ctgcctgcct 240  
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t 301

<210> 300

<211> 301

<212> DNA

<213> Homo sapien

&lt;400&gt; 300

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gctgcattcc	acaaggttct	cagcctaata	agtttacta	cctgccagtc	tcaaaactta	180
gtaaagcaag	accatgacat	tccccacgg	aaatcagagt	ttgcccacc	gtcttggtac	240
tataaagcct	gcctctaaca	gtccttgctt	cttcacacca	atcccagagc	catcccccat	300
g						301

&lt;210&gt; 301

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 301

ttaaattttt	gagaggataa	aaaggacaaa	taatctagaa	atgtgtcttc	ttcagtctgc	60
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gggaactcac	aaagaccctc	agagctgaga	caccacaaac	agtgggagct	cacaaagacc	180
ctcagagctg	agacacccac	aacagtggga	gtcacaaaag	accctcagag	ctgagacacc	240
cacaacagca	cctcgttcag	ctgccacatg	tgtgaataag	gatgcaatgt	ccagaagtgt	300
t						301

&lt;210&gt; 302

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 302

aggtacacat	ttagcttggt	gtaaatgact	cacaaaactg	attttaaaat	caagttaatg	60
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ttgagttggg	tcttagtatt	atztatggta	aataggctct	taccacttgc	aaataactgg	180
ccacatcatt	aatgactgac	ttcccagtaa	ggctctctaa	ggggtaagta	ggaggatcca	240
caggatttga	gatgctaagg	ccccagagat	cgtttgatcc	aaccctctta	ttttcagagg	300
g						301

&lt;210&gt; 303

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 303

aggtaccaac	tgtggaaata	ggtagaggat	cattttttct	ttccatatca	actaagttgt	60
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tggctaattg	aactaccgct	tgcagttaa	aaatgggtgg	ttgtgaaatg	atcataggcc	180
agtaacgggt	atgtttttct	aactgatctt	ttgctcgttc	caaagggacc	tcaagacttc	240
catcgatttt	atatctgggg	tctagaaaag	gagttaatct	gttttccctc	ataaattcac	300
c						301

&lt;210&gt; 304

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 304

acatggatgt	tattttgcag	actgtcaacc	tgaatttgta	tttgcttgac	attgcctaatt	60
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tattagtttc agtttcagct taccactttt ttgtctgcaa catgcaraas agacagtgcc 120  
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 gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga 240  
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 c 301

<210> 305  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

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 taaaggagga gaaacagata caaatctcc aactcagtat taaggatttc tcatgcctag 180  
 aatattggta gaaacaagaa tacattcata tggcaaataa ctaaccatgg tggaaacaaa 240  
 ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag 300  
 a 301

<210> 306  
 <211> 8  
 <212> PRT  
 <213> Homo sapien

<400> 306  
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 1 5

<210> 307  
 <211> 637  
 <212> DNA  
 <213> Homo sapien

<400> 307  
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 attgaggaat gatacttgag cccaaagagc attcaatcat tgttttattt gccttmtttt 180  
 cacaccattg gtgagggagg gattaccacc ctggggttat gaagatgggt gaacaccca 240  
 cacatagcac cgagatatg agatcaacag tttcttagcc atagagattc acagcccaga 300  
 gcaggaggac gcttgcacac catgcaggat gacatggggg atgcgctcgg gattggtgtg 360  
 aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacggtgggg caaactctga 420  
 tttccgtggg ggaatgtcat ggtcttgctt tactaagttt tgagactggc aggtagtga 480  
 actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca 540  
 ggtgggagcc tttcccagtg ggtgtgggac atatctggca agattttgtg gcactcctgg 600  
 ttacagatac tggggcagca aataaaaactg aatcttg 637

<210> 308  
 <211> 647  
 <212> DNA  
 <213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(647)  
<223> n = A,T,C or G

<400> 308  
acgattttca ttatcatgta aatcggttca ctcaaggggc caaccacagc tgggagccac 60  
tgctcagggg aaggttcata tgggactttc tactgcccaa gggtctatac aggatataaa 120  
ggngcctcac agtatagatc tggtagcaaa gaagaagaaa caaacactga tctctttctg 180  
ccaccctctt gacccttttg aactcctctg accctttaga acaagcctac ctaatatctg 240  
ctagagaaaa gaccaacaac ggctctcaag gatctcttac catgaaggtc tcagctaatt 300  
cttgggctaag atgtgggttc cacattaggc tctgaatatg gggggaaggg tcaatttgct 360  
cattttgtgt gtggataaag tcaggatgcc caggggccag agcagggggc tgcttgcttt 420  
gggaacaatg gctgagcata taaccatagg ttatggggaa caaaacaaca tcaaagtcac 480  
tgtatcaatt gccatgaaga cttgagggac ctgaatctac cgattcatct taaggcagca 540  
ggaccagttt gagtggcaac aatgcagcag cagaatcaat ggaaacaaca gaatgattgc 600  
aatgtccttt tttttctcct gcttctgact tgataaaagg ggaccgt 647

<210> 309  
<211> 460  
<212> DNA  
<213> Homo sapien

<400> 309  
actttatagt ttaggctgga cattggaaaa aaaaaaaagc cagaacaaca tgtgatagat 60  
aatatgattg gctgcacact tccagactga tgaatgatga acgtgatgga ctattgtatg 120  
gagcacatct tcagcaagag ggggaaatac tcatcatttt tggccagcag ttgtttgatc 180  
accaaacatc atgccagaat actcagcaaa ccttcttagc tcttgagaag tcaaagtccg 240  
ggggaattta ttcttgcaa ttttaattgg actccttatg tgagagcagc ggctaccag 300  
ctgggggtgt ggagcgaacc cgtcactagt ggacatgcag tggcagagct cctggttaacc 360  
acctagagga atacacaggc acatgtgtga tgccaagcgt gacacctgta gcactcaaat 420  
ttgtcttgtt tttgtctttc ggtgtgtaag attcttaagt 460

<210> 310  
<211> 539  
<212> DNA  
<213> Homo sapien

<400> 310  
acgggactta tcaaataaag ataggaaaag aagaaaactc aaatattata ggcagaaatg 60  
ctaaaggttt taaaatatgt caggattgga agaaggcatg gataaagaac aaagttcagt 120  
taggaaagag aaacacagaa ggaagagaca caataaaagt cattatgtat tctgtgagaa 180  
gtcagacagt aagatttgtg ggaaatgggt tggtttgttg tatggtatgt attttagcaa 240  
taatctttat ggcagagaaa gctaaaatcc tttagcttgc gtgaatgatc acttgctgaa 300  
ttcctcaagg taggcatgat gaaggagggt ttagaggaga cacagacaca atgaactgac 360  
ctagatagaa agccttagta tactcagcta ggaatagtga ttctgagggc aactgtgac 420  
atgattatgt cttacatgt atggtagtga tggggatgat aggaagggaag aacttatggc 480  
atattttcac ccccaaaaa gtcagttaaa tattgggaca ctaaccatcc aggtcaaga 539

<210> 311  
<211> 526  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(526)  
<223> n = A,T,C or G

<400> 311  
caaatattgag ccaatgacat agaattttac aaatcaagaa gcttattctg gggccatttc 60  
ttttgacgtt ttctctaaac tactaaagag gcattaatga tccataaatt atattatcta 120  
catttacagc atttaaaatg tggtcagcat gaaatattag ctacagggga agctaaataa 180  
attaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg 240  
tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa 300  
aaaatgggga aactctgaag gggttttaagt atcttacctg aagctacaga ctccataacc 360  
tctctttaca gggagctcct gcagccccta cagaaatgag tggctgagat tcttgattgc 420  
acagcaagag cttctcatct aaaccctttc ccttttttagt atctgtgtat caagtataaa 480  
agttctataa actgtagtnt acttatttta atcccaaaag cacagt 526

<210> 312  
<211> 500  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(500)  
<223> n = A,T,C or G

<400> 312  
cctctctctc cccaccccct gactctagag aactgggttt tctcccagta ctccagcaat 60  
tcattttctga aagcagttga gccactttat tccaaagtac actgcagatg ttcaaactct 120  
ccattttctct ttcccttcca cctgccagtt ttgctgactc tcaacttgct atgagtgtaa 180  
gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg 240  
gcttcttagg aaaatatttt tcttccaaaa tcagtaggaa atctaaactt atcccctctt 300  
tgcagatgtc tagcagcttc agacatttgg ttaagaacct atgggaaaaa aaaaaatcct 360  
tgctaattgt gtttcctttg taaaccanga ttcttatttg nctggtatag aatatcagct 420  
ctgaacgtgt ggtaaagatt tttgtgtttg aatataggag aaatcagttt gctgaaaagt 480  
tagtcttaat tatctattgg 500

<210> 313  
<211> 718  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(718)  
<223> n = A,T,C or G

<400> 313  
ggagatttgt gtggtttgca gccgagggag accaggaaga tctgcatggt gggaaggacc 60  
tgatgatata gaggtgagaa ataagaaagg ctgctgactt taccatctga ggccacacat 120  
ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa 180  
gtagtgcacat gtttttgcac atttccagcc cttttaaata tccacacaca caggaagcac 240  
aaaaggaagc acagagatcc ctgggagaaa tgcccggccg ccattctggg tcatcgatga 300  
gcctcgccct gtgcctgntc ccgcttgtga gggaaggaca ttagaaaatg aattgatgtg 360  
ttccttaaag gatggcagga aaacagatcc tggtgtggat atttatttga acgggattac 420

agatttgaaa tgaagtcaca aagtgagcat taccaatgag aggaaaacag acgagaaaat	480
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aactggggag gagataccac ggggcagagg tcaggattct ggccctgctg cctaactgtg	600
cgttatacca atcatttcta tttctaccct caaacaagct gtngaataac tgacttacgg	660
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&lt;210&gt; 314

&lt;211&gt; 358

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 314

gtttatttac attacagaaa aaacatcaag acaatgtata ctatttcaaa tatatccata	60
cataatcaaa tatagctgta gtacatgttt tcattgggtg agattaccac aaatgcaagg	120
caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa	180
gctctcggtg gtccagccac tgtgaaacat gtcctcttta gattaacctc gtggacgctc	240
ttgttgatt gctgaactgt agtgccctgt attttgcttc tgtctgtgaa ttctgttgct	300
tctggggcat ttccttggtg tgcagaggac caccacacag atgacagcaa tctgaatt	358

&lt;210&gt; 315

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 315

taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc	60
ataggtgatg atgaggacat ggaatgggcc cccaaggatg gtctgtccaa agaagcgagt	120
gaccccatc ctgaagatgt ctggaacctc taccagcagg atgatgatag cccaatgac	180
agtcaccagc tccccgacca gccggatata gtccttaggg gtcatgtagg cttcctgaag	240
tagcttctgc tgtaagaggg tgttgctccg ggggctcgtg cggttattgg tctgggctt	300
gagggggcgg tagatgcagc acatggtgaa gcagatgatg t	341

&lt;210&gt; 316

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 316

agactgggca agactcttac gccccacact gcaatttggt cttgttgccg tatccattta	60
tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact	120
cattcagggg gctctgggtg caatattagt t	151

&lt;210&gt; 317

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 317

agaactagtg gatcctaag aaataacctga aacatatatt ggcatttatc aatgggtcaa	60
atcttcattt atctctggcc ttaacctgg ctcctgaggc tgcggccagc agatcccagg	120
ccagggtctt gttcttgcca cactgcttg a	151

&lt;210&gt; 318

&lt;211&gt; 151

&lt;212&gt; DNA

<213> Homo sapien

<400> 318

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actggtggga ggcgctgttt agttggctgt tttcagaggg gtctttcgga gggacctcct    60
gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg    120
tgggggcggt ttatcaggca gtgataaaca t                                     151
```

<210> 319

<211> 151

<212> DNA

<213> Homo sapien

<400> 319

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aactagtggga tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta    60
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg    120
taagattggg tttatgtgat tttagtgggt a                                     151
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<210> 320

<211> 150

<212> DNA

<213> Homo sapien

<400> 320

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aactagtggga tccactagtc cagtgtgggt gaattccatt gtgttggggt tctagatcgc    60
gagcggctgc cctttttttt tttttttttg ggggggaatt tttttttttt aatagttatt    120
gagtgttcta cagcttacag taaataccat                                     150
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<210> 321

<211> 151

<212> DNA

<213> Homo sapien

<400> 321

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agcaactttg tttttcatcc aggttatttt aggcttagga tttcctctca cactgcagtt    60
taggggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg    120
tgctcttgag aaatcaaagt cttcatacac t                                     151
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<210> 322

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 322

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tttgggcttg gtcagtttgc cacagggtt ggagatgggt acagtcttct ggcattcggc    120
attgtgcagg gctcgcttca nacttccagt t                                     151
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<210> 323

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 323

tgaggacttg	tkttcttttt	ctttattttt	aatcctctta	ckttgtaa	atattgccta	60
nagactcant	tactaccag	tttgtggtt	twtgaggaa	atgtaactg	acagttagct	120
gttcaatyaa	aaagacactt	ancccatgtg	g			151

<210> 324

<211> 461

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(461)

<223> n = A,T,C or G

<400> 324

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agaagtggc	agctaaagga	atccagggtg	ttgggtggac	tgtaataacc	tttgatgaaa	120
agagttacta	cgaatcccat	cttggttcca	gctatatcac	tgacagcatg	gtagaagact	180
gcgaacctca	cttctagact	ttcacgggtg	gacgaaacgg	gttcagaaac	tgccaggggc	240
ctcatacagg	gatataaaaa	taccctttgt	gctaccagg	ccctggggaa	tcaggtgact	300
cacacaaatg	caatagtgtg	tactgcatt	tttacctgaa	ccaaagctaa	acccgggtgt	360
gccaccatgc	accatggcat	gccagagttc	aacactgttg	ctcttgaaaa	ttgggtctga	420
aaaaacgcac	aagagcccct	gccctgccct	agctgangca	c		461

<210> 325

<211> 400

<212> DNA

<213> Homo sapien

<400> 325

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tttgatgtct	ccaagtagtc	caccttcatt	taactctttg	aaactgtatc	atctttgcca	120
agtaagagtg	gtggcctatt	tcagctgctt	tgacaaaatg	actggctcct	gacttaacgt	180
tctataaatg	aatgtgctga	agcaaagtgc	ccatgggtggc	ggcgaagaag	agaaagatgt	240
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gtcccttttg	cattgccaag	tgccataacc	atgagcacta	cgctaccatg	gttctgcctc	360
ctggccaagc	aggctgggtt	gcaagaatga	aatgaatgat			400

<210> 326

<211> 1215

<212> DNA

<213> Homo sapien

<400> 326

ggaggactgc	agcccgact	cgcagccctg	gcaggcggca	ctggctcatg	aaaacgaatt	60
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gaactcctac	accatcgggc	tgggcctgca	cagtcttgag	gccgaccaag	agccagggag	180

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ccagatggtg gaggccagcc tctccgtacg gcacccagag tacaacagac ccttgctcgc 240
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aaaaaaaaa aaaaaa 1215

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&lt;210&gt; 327

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 327

```

Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
1           5           10           15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
20          25          30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
35          40          45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
50          55          60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
65          70          75          80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
85          90          95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
100         105         110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
115         120         125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
130         135         140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
145         150         155         160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
165         170         175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
180         185         190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
195         200         205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
210         215         220

```

&lt;210&gt; 328

<211> 234  
 <212> DNA  
 <213> Homo sapien

<400> 328  
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 atccgcagtg ggtgctgtca gccacacact gtttccagaa ctcctacacc atcgggctgg 180  
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<210> 329  
 <211> 77  
 <212> PRT  
 <213> Homo sapien

<400> 329  
 Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser  
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 Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu  
 20 25 30  
 Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr  
 35 40 45  
 His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu  
 50 55 60  
 Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala  
 65 70 75

<210> 330  
 <211> 70  
 <212> DNA  
 <213> Homo sapien

<400> 330  
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 gctgcagcca 70

<210> 331  
 <211> 22  
 <212> PRT  
 <213> Homo sapien

<400> 331  
 Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu  
 1 5 10 15  
 Val Ser Gly Ser Cys Ser  
 20

<210> 332  
 <211> 2507  
 <212> DNA  
 <213> Homo sapien

<400> 332  
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gtacatcaac	tgttcagctt	cctgggaaaag	tagttgtggt	cacaggagct	aatacaggta	180
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actagttaag	gattaatagc	aaaagayatt	aaatatgcta	acatagctat	ggaggaattg	1860
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&lt;210&gt; 333

&lt;211&gt; 3030

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 333

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&lt;210&gt; 334

&lt;211&gt; 2417

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 334

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&lt;210&gt; 335

&lt;211&gt; 2984

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 335

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&lt;210&gt; 336

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 336

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Leu	Asp	Ser	Glu	Asn	Thr	Ser	Gly	Ala	Leu	Pro	Arg	Leu	Pro	Gln	Thr
			20					25					30		
Pro	Lys	Gln	Pro	Gln	Lys	Arg	Ser	Arg	Ala	Ala	Phe	Ser	His	Thr	Gln
		35				40						45			
Val	Ile	Glu	Leu	Glu	Arg	Lys	Phe	Ser	His	Gln	Lys	Tyr	Leu	Ser	Ala
	50				55					60					
Pro	Glu	Arg	Ala	His	Leu	Ala	Lys	Asn	Leu	Lys	Leu	Thr	Glu	Thr	Gln
65					70					75					80

Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln  
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 Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala  
                             100                            105                            110  
 Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn  
                             115                            120                            125  
 Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro  
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 Ala Phe Trp  
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 <212> PRT  
 <213> Homo sapien

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<210> 338  
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 <212> PRT  
 <213> Homo sapien

<400> 338  
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<210> 339  
 <211> 318  
 <212> PRT  
 <213> Homo sapien

<400> 339  
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 Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val  
                             20                            25                            30  
 Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly  
                             35                            40                            45  
 Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg  
   50                            55                            60  
 Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu  
  65                            70                            75                            80  
 Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val  
                             85                            90                            95  
 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys  
                             100                            105                            110  
 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala  
                             115                            120                            125  
 Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met  
                             130                            135                            140  
 His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu

145                      150                      155                      160  
 Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser  
                          165                      170                      175  
 Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly  
                          180                      185                      190  
 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala  
                          195                      200                      205  
 Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly  
                          210                      215                      220  
 Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val  
                          225                      230                      235                      240  
 Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe  
                          245                      250                      255  
 Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu  
                          260                      265                      270  
 Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His  
                          275                      280                      285  
 Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg  
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 Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp  
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&lt;210&gt; 340

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 340

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&lt;210&gt; 341

&lt;211&gt; 344

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 341

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 aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc 300  
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&lt;210&gt; 342

&lt;211&gt; 592

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 342

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cccgtgtcct	tatgcaata	atcgtcttct	tctaaatttc	tcctaggctt	cattttccaa	480
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&lt;210&gt; 343

&lt;211&gt; 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 343

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&lt;210&gt; 344

&lt;211&gt; 536

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 344

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&lt;210&gt; 345

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 345

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gtgccatttc	c					251

<210> 346  
 <211> 282  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
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 <223> n = A,T,C or G

<400> 346  
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 agggagacta tacctggctc ttgccctaag tgagagggtc tccctcccg accaaaaaat 180  
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<220>  
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 <223> n = A,T,C or G

<400> 347  
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 tctgagactg actggaccca cccagaccca gggcaaagat acatgttacc atatcatctt 180  
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<400> 348  
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 aggagacact cccagcatgg aggagggtt atcttttcat cctaggtcag gtctacaatg 180  
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 gccctgctc c 251

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 <211> 251  
 <212> DNA  
 <213> Homo sapien

<400> 349  
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 cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt 180  
 agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca 240



actcctggtt t

251

&lt;210&gt; 350

&lt;211&gt; 908

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 350

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aatcgcag						908

&lt;210&gt; 351

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 351

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gatctgtcca	caacaaactt	gccctctcat	gccttgcttc	tcaccatgct	ctgctccagg	360
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&lt;210&gt; 352

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 352

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aataagcaca	a					251

&lt;210&gt; 353

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 353

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ttaacagaat	actagattca	cactggaacg	ggggtaaaga	agaaattatt	ttctataaaa	420
gggctcctaa	tgtagt					436

&lt;210&gt; 354

&lt;211&gt; 854

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 354

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&lt;210&gt; 355

&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 355

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&lt;210&gt; 356

&lt;211&gt; 574

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 356

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&lt;210&gt; 357

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 357

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&lt;210&gt; 358

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 358

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&lt;210&gt; 359

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 359

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&lt;210&gt; 360

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 360

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&lt;210&gt; 361

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 361

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&lt;210&gt; 362

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 362

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&lt;210&gt; 363

&lt;211&gt; 653

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(653)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 363

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cccgtccag attccctcag acctttgccg gtcccattat tggctstggt ggt	653

&lt;210&gt; 364

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 364

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catttcacac cttcatata aattcactat cttggcttga ggcactccat aaaatgtatc	300
acgtgcatag taaatcttta tatttgctat ggcgttgac tagaggactt ggactgcaac	360
aagtggatgc gcggaaaatg aaatcttctt caatagccca g	401

&lt;210&gt; 365

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 365

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&lt;210&gt; 366

&lt;211&gt; 1851

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 366

tcacacccat tgccagcagc ggcaccgtta gtcaggtttt ctgggaatcc cacatgagta	60
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ttgctgtttt	cagaagagat	ttttaacatc	tgtttttctt	tgtagtcaga	aagtaactgg	240
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&lt;210&gt; 367

&lt;211&gt; 668

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 367

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aaaaaaaa						668

&lt;210&gt; 368

&lt;211&gt; 1512

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 368

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gaacatggca	ctgatccaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
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actccaagaa	aagttaaaca	tgtttcagtg	aatagagatc	ctgctccttt	ggcaagttcc	1440
taaaaaacag	taatagatac	gagggtgatgc	gcctgtcagt	ggcaagggtt	aagatatttc	1500
tgatctcgtg	cc					1512

&lt;210&gt; 369

&lt;211&gt; 1853

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 369

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&lt;210&gt; 370

&lt;211&gt; 2184

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 370

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<210> 371  
 <211> 1855  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(1855)  
 <223> n = A,T,C or G

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 <212> DNA  
 <213> Homo sapien

<400> 372  
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 gcgcttgrgg agactmcgat gacagygcct tcatggagcc cagggtaccac gtccgtggag 180  
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caacttaatg	tccttgacaa	caaaaagagg	acagctctga	yaaaggccgt	acaatgccag	420
gaagatgaat	gtgctgtaat	gttgcctgaa	catggcactg	atccaaatat	tccagatgag	480
tatggaaata	ccactctrca	ctaygctrct	tayaatgaag	ataaattaat	ggccaaagca	540
ctgctcttat	ayggtgctga	tatcgaatca	aaaaacaagg	tatagatcta	ctaattttat	600
cttcaaaata	ctgaaatgca	ttcattttta	cattgacgtg	tgttaagggcc	agtcttccgt	660
atgttggaagc	tcaagcataa	cttgaatgaa	aataattttga	aatgacctaa	ttatctaaga	720
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&lt;210&gt; 373

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 373

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accagaaata	aataa					1155

&lt;210&gt; 374

&lt;211&gt; 2000

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 374

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tgggtgctgcc	actgcttccc	ctgctgcagg	gggagcggca	agagcaaggt	gggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccaggatcc	acgtccgtgg	agaagatctg	420
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ctcagggaca	ctgacgtgaa	caagaaggac	aaagcaaaaaga	ggactgctct	acatctggcc	540

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aaaaaaaaaa	aaaaaaaaaa					2000

&lt;210&gt; 375

&lt;211&gt; 2040

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 375

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gaaaaagaca tcttgcatga aaatagtacg ttgcgggaag aaattgccat gctaagactg 1980
gagctagaca caatgaaaca tcagagccag ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040

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&lt;210&gt; 376

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 376

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1      5      10      15
Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
20     25     30
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
35     40     45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
50     55     60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65     70     75     80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
85     90     95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
100    105    110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
115    120    125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
130    135    140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145    150    155    160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
165    170    175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
180    185    190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
195    200    205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
210    215    220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225    230    235    240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
245    250    255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
260    265    270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
275    280    285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu

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290                      295                      300  
 Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu  
 305                      310                      315                      320  
 Ser Met Leu Phe Leu Val Ile Ile Met  
                     325

<210> 377  
 <211> 148  
 <212> PRT  
 <213> Homo sapien

<220>  
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                     20                      25                      30  
 Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys  
                     35                      40                      45  
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu  
 50                      55                      60  
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp  
 65                      70                      75                      80  
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp  
                     85                      90                      95  
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro  
                     100                      105                      110  
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp  
                     115                      120                      125  
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser  
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 Lys Asn Lys Val  
 145

<210> 378  
 <211> 1719  
 <212> PRT  
 <213> Homo sapien

<400> 378  
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 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
                     35                      40                      45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50                      55                      60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65                      70                      75                      80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn

				85					90					95		
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	
			100					105					110			
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe	
		115					120					125				
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His	
		130				135					140					
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met	
145					150					155					160	
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala	
				165					170						175	
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu	
		180						185					190			
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr	
		195					200					205				
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met	
		210				215					220					
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn	
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Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys	
				245					250					255		
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly	
			260					265					270			
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val	
		275					280					285				
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr	
	290					295					300					
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile	
305					310					315					320	
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu	
				325					330					335		
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val	
			340					345					350			
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile	
		355					360					365				
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Asn	Val	Ser	Arg	Thr	Arg	Asn	Lys	
	370					375					380					
Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser	
385					390					395					400	
Ser	Val	Lys	Lys	Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	
				405					410					415		
Cys	Arg	Cys	Phe	Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	
			420													

Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp  
 530 535 540  
 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln  
 545 550 555 560  
 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val  
 565 570 575  
 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn  
 580 585 590  
 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu  
 595 600 605  
 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp  
 610 615 620  
 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys  
 625 630 635 640  
 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys  
 645 650 655  
 Asn Lys His Gly Leu Thr Pro Leu Leu Gly Val His Glu Gln Lys  
 660 665 670  
 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala  
 675 680 685  
 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly  
 690 695 700  
 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser  
 705 710 715 720  
 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser  
 725 730 735  
 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln  
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 Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys  
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 770 775 780  
 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp  
 785 790 795 800  
 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly  
 805 810 815  
 Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn  
 820 825 830  
 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe  
 835 840 845  
 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser  
 850 855 860  
 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn  
 865 870 875 880  
 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu  
 885 890 895  
 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile  
 900 905 910  
 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn  
 915 920 925  
 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro  
 930 935 940  
 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu  
 945 950 955 960  
 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe

965 970 975  
 Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His  
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 Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser  
 995 1000 1005  
 Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu  
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 Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His  
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 Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg  
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 Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val  
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 Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys  
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 1250 1255 1260  
 Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro  
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 1285 1290 1295  
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 1365 1370 1375  
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr  
 1380 1385 1390  
 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr  
 1395 1400 1405



Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu  
 1410 1415 1420  
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly  
 1425 1430 1435 144  
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Ser Gln Glu Pro Glu Ile Asn  
 1445 1450 1455  
 Lys Asp Gly Asp Arg Glu Val Glu Glu Met Lys Lys His Glu Ser  
 1460 1465 1470  
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly  
 1475 1480 1485  
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu  
 1490 1495 1500  
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys  
 1505 1510 1515 152  
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser  
 1525 1530 1535  
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu  
 1540 1545 1550  
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser  
 1555 1560 1565  
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe  
 1570 1575 1580  
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe  
 1585 1590 1595 160  
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly  
 1605 1610 1615  
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro  
 1620 1625 1630  
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln  
 1635 1640 1645  
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile  
 1650 1655 1660  
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser  
 1665 1670 1675 168  
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn  
 1685 1690 1695  
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr  
 1700 1705 1710  
 Met Lys His Gln Ser Gln Leu  
 1715

&lt;210&gt; 379

&lt;211&gt; 656

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 379

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1 5 10 15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
 20 25 30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50 55 60

Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 85 90 95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 100 105 110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 115 120 125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 130 135 140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145 150 155 160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 165 170 175  
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 180 185 190  
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 195 200 205  
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 210 215 220  
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn  
 225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val  
 340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile  
 355 360 365  
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu  
 370 375 380  
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys  
 385 390 395 400  
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu  
 405 410 415  
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn  
 420 425 430  
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro  
 435 440 445  
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu  
 450 455 460  
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu  
 465 470 475 480  
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp  
 485 490 495  
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu

Asn	Gly	Gln	Pro	Glu	Leu	Glu	Asn	Phe	Met	Ala	Ile	Glu	Glu	Met	Lys
	515						520					525			
Lys	His	Gly	Ser	Thr	His	Val	Gly	Phe	Pro	Glu	Asn	Leu	Thr	Asn	Gly
	530						535					540			
Ala	Thr	Ala	Gly	Asn	Gly	Asp	Asp	Gly	Leu	Ile	Pro	Pro	Arg	Lys	Ser
545						550					555				560
Arg	Thr	Pro	Glu	Ser	Gln	Gln	Phe	Pro	Asp	Thr	Glu	Asn	Glu	Glu	Tyr
			565						570					575	
His	Ser	Asp	Glu	Gln	Asn	Asp	Thr	Gln	Lys	Gln	Phe	Cys	Glu	Glu	Gln
			580						585				590		
Asn	Thr	Gly	Ile	Leu	His	Asp	Glu	Ile	Leu	Ile	His	Glu	Glu	Lys	Gln
		595					600					605			
Ile	Glu	Val	Val	Glu	Lys	Met	Asn	Ser	Glu	Leu	Ser	Leu	Ser	Cys	Lys
	610					615					620				
Lys	Glu	Lys	Asp	Ile	Leu	His	Glu	Asn	Ser	Thr	Leu	Arg	Glu	Glu	Ile
625					630					635					640
Ala	Met	Leu	Arg	Leu	Glu	Leu	Asp	Thr	Met	Lys	His	Gln	Ser	Gln	Leu
				645					650					655	

&lt;210&gt; 380

&lt;211&gt; 671

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 380

Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser	Ser	Val	Lys	Lys
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Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe
			20					25					30		
Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp
		35					40					45			
His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp
	50					55					60				
Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val
65					70					75				80	
Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn
			85					90					95		
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser
		100						105					110		
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe
		115					120					125			
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His
	130					135					140				
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met
145					150					155				160	
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala
			165						170					175	
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu
		180					185						190		
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr
		195					200					205			
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met
210						215					220				
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn

225						230					235					240
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys	
				245					250						255	
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly	
			260					265						270		
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val	
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Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr	
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Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile	
305					310					315					320	
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu	
			325						330					335		
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val	
			340					345					350			
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile	
		355					360					365				
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu	
	370					375					380					
Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser	Gln	Pro	Glu	Lys	
385					390					395					400	
Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp	Arg	Glu	Val	Glu	
			405						410					415		
Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly	Leu	Leu	Glu	Asn	
			420					425					430			
Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn	Gly	Leu	Ile	Pro	
		435					440					445				
Gln	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Asn	Gln	Gln	Phe	Pro	Asp	Asn	Glu	
	450					455					460					
Ser	Glu	Glu	Tyr	His	Arg	Ile	Cys	Glu	Leu	Val	Ser	Asp	Tyr	Lys	Glu	
465					470					475					480	
Lys	Gln	Met	Pro	Lys	Tyr	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	
			485						490					495		
Leu	Lys	Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Leu	Glu	Gly	Ser	Glu	
			500					505					510			
Asn	Gly	Gln	Pro	Glu	Lys	Arg	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	
		515					520					525				
Gly	Asp	Arg	Glu	Leu	Glu	Asn	Phe	Met	Ala	Ile	Glu	Glu	Met	Lys	Lys	
	530					535					540					
His	Gly	Ser	Thr	His	Val	Gly	Phe	Pro	Glu	Asn	Leu	Thr	Asn	Gly	Ala	
545					550					555					560	
Thr	Ala	Gly	Asn	Gly	Asp	Asp	Gly	Le								

<210> 381  
<211> 251  
<212> DNA  
<213> Homo sapien

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ccaatatccc aggagaagca ttggggagtt gggggcaggt gaaggacca ggactcacac 180  
atcctggggc tccaaggcag aggagaggggt cctcaagaag gtcaggagga aaatccgtaa 240  
caagcagtca g 251

<210> 382  
<211> 3279  
<212> DNA  
<213> Homo sapiens

<400> 382  
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atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtgt 120  
cactgggagg ggacatcctg cagaaggttag gagtgcagca acacccgctg caggggaggg 180  
gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240  
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cagggcgcca gatggcctca cacaggaag agagggcccc tctgcaggg cctcacctgg 360  
gccacaggag gacactgctt ttctctgtag gagtgcaggag ctgtgagatg tgctggacag 420  
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cctcagtcct tcccctccac tccatcctcc atctggcctc agtgggtcat tctgactact 660  
gaactgacca taccagccc tgcccacggc cctccatggc tcccaatgc cctggagagg 720  
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gtagctgac cagctgatag aggaactagc caggtggggg cctttccctt tggatggggg 2160

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gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
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gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtttt 3279

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&lt;210&gt; 383

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 383

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Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
      5              10              15

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
      20              25              30

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
      35              40              45

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
      50              55              60

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
      65              70              75              80

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
      85              90              95

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
      100             105             110

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
      115             120             125

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
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Ala Leu Glu Arg Gly His Leu Val Arg Glu
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<211> 557  
<212> DNA  
<213> Homo sapiens

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ggggaagggt cccttttgca ttgccaagt ccataacat gagcactact ctaccatggt 180  
tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240  
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ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360  
tccccaagac acatcctaaa aggtgttgta atgggtgaaaa cgtcttcctt ctttattgcc 420  
ccttcttatt tatgtgaaca actgtttgc tttttttgta tcttttttaa actgtaaaagt 480  
tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttcc aaagtaaaaa 540  
aaaaaaaaa aaaaaaa 557

<210> 385  
<211> 337  
<212> DNA  
<213> Homo sapiens

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tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180  
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240  
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ctttggccac caattcccc ttttccacat cccggca 337

<210> 386  
<211> 300  
<212> DNA  
<213> Homo sapiens

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gcgaccttgg ccgaaggct ctacgaagga cccaccgacc ccagccgcgg cggcggcggc 180  
gcggactttg ccggtgtgt ggggcgggagc ggactgctg tccgcggacg ggcagcgaag 240  
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<210> 387  
<211> 537  
<212> DNA  
<213> Homo sapiens

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tgaaccagga ccggcttctg ggcggctgaa aggggcaagg aggcaaggac cccgtctctc 180  
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttctc agcactgagg 240  
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gcggcccagc acttcctcag acacaacttc ttcttctgtc tccagtcgtg gggatcatca 360  
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gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctccagcctgg ttagtctcc 480  
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<210> 388

<211> 520

<212> DNA

<213> Homo sapiens

<400> 388

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tcatactcaa ttgatgggta ttagacaatt ccatttcttt ctgggttatra taaacagaaa 420  
atctttctct ttctcattac cagtaaaggc tcttggtatc tttctgttgg aatgatttct 480  
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<210> 389

<211> 365

<212> DNA

<213> Homo sapiens

<400> 389

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aacgactttc caaataatct caccagcgc ttccagctca ggcgtcctag aagcgtcttg 180  
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240  
cccaggaaac cttcagacta ccttctctg ccttcagcaa ggggcgttgc ccacattctc 300  
tgagggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360  
gggag 365

<210> 390

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(221)

<223> n = A,T,C or G

<400> 390

tgctctcca tcttgcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60  
tacacggnnt ctcatgggtg tggaacatct ctgcttgagg ttccaggaag gcctctggct 120  
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180  
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

<210> 391

<211> 325

<212> DNA

<213> Homo sapiens



<220>  
<221> misc\_feature  
<222> (1)...(325)  
<223> n = A,T,C or G

<400> 391  
tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60  
ctctcgcgcc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120  
tagccagggc actgctgcc aacagccagtc cnnataccat catgtnaccc ggtgngctct 180  
naanttngat ntccanagcc ctacccatcn tagttctgct ctcccaccgg ntaccagccc 240  
cactgcccag gaatcctaca gccagtaccc tgtcccgacg tctctaccta ccagtacgat 300  
gagacctccg gctactacta tgacc 325

<210> 392  
<211> 277  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(277)  
<223> n = A,T,C or G

<400> 392  
atattgttta actccttcct ttatatcttt taacattttc atggngaaaag gttcacatct 60  
agtctcactt nggcnagnn ctctacttg agtctcttcc ccggcctggn ccagtngnaa 120  
antaccanga accgncatgn cttaanaacn ncctggtttn tgggttnntc aatgactgca 180  
tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240  
ctgaggatac agcgccgcgt cctgtgttgc tggggaa 277

<210> 393  
<211> 566  
<212> DNA  
<213> Homo sapiens

<400> 393  
actagtccag tgtggtggaa ttcgcgcccg cgtcgacgga caggtcagct gtctggctca 60  
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga tttaaattcag cctaaacgtt 120  
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcccggca 180  
gagaaggctc agtttgtcca tcagcattat catgatatca ggactgggta cttgggttaag 240  
gaggggtcta ggagatctgt cccttttaga gacaccttac ttataatgaa gtatttggga 300  
gggtggtttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360  
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420  
ttctgcctca atgtttactg tgcctttggt tttgctagtt tgtgtgtgtg aaaaaaaaaa 480  
cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540  
ttttgcctat caaaaaaaaa aaaaaa 566

<210> 394  
<211> 384  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

```
gaacatacat gtccccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaattn gaccggggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggctttta ggagttttta gctgagtgtc actgtagacc ccaaatacca 180
tccaagatt atcgggagaa agggggcagt aattacccaa atccggttgg agcatgacgt 240
gaacatccag ttctctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300
agggtagcaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt 384
```

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

```
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgc 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcatt cggaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcagctct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggg 360
gcagcctggt gagaccatcc aatcccaaat aaaatgcac 399
```

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

```
tggagtntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttagggga gggagtgagg gataaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgtag gccctgctct ttt 403
```

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(100)

<223> n = A,T,C or G

&lt;400&gt; 397

actagtnacag tgtgggtggaa ttcgcgcccg cgctcgaccta naanccatct ctatagcaaa 60  
tccatccccg ctcttggttg gtnacagaat gactgacaaa 100

&lt;210&gt; 398

&lt;211&gt; 278

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(278)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 398

gcggccgcgt cgacagcagt tccgccagcg ctgcgccctg ggtggggatg tgctgcacgc 60  
ccacctggac atctggaagt cagcgccctg gatgaaagag cggacttcac ctggggcgat 120  
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgaggtgg actcatcatg 180  
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240  
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

&lt;210&gt; 399

&lt;211&gt; 298

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(298)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 399

acggaggtgg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60  
ggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120  
ccgagatcga gcgcatgggc ctggatcatg accgcatggg ctccgtggag cgcgtgggct 180  
ccggcattga gcgcatgggc ccgctgggcc tcgaccacat ggctccanc attgancgca 240  
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcattggg 298

&lt;210&gt; 400

&lt;211&gt; 548

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 400

acatcaacta cttcctcatt ttaaggtatg gcagttccct tcatccccctt ttctgcctt 60  
gtacatgtac atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaagg 120  
caaagaacca cagccttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180  
tgagtctctt ttttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac 240  
tgacagagggc tagagaatta tttcatacag gctttgaggc caccatgtc acttatccc 300  
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360  
gttggcccca taattctggg cttttgttgt ttgttttaat tacttgggca tcccaggaag 420  
ctttccagtg atctctacc atgggcccc ctctgggat caagccctc ccaggccctg 480  
tccccagccc ctctgcccc agcccaccg cttgccttgg tgctcagccc tccattggg 540  
agcagggtt 548

<210> 401  
<211> 355  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(355)  
<223> n = A,T,C or G

<400> 401  
actgtttcca tggtatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60  
tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120  
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180  
tataaatgaa tgtgctgaag caaagtgcc atgggtggcg cgaagaagan aaagatgtgt 240  
tttgttttgg actctctgtg gtcccttcca atgctgnggg tttccaacca ggggaagggt 300  
cccttttgca ttgccaaagt ccataaccat gagcactact ctaccatggn tctgc 355

<210> 402  
<211> 407  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(407)  
<223> n = A,T,C or G

<400> 402  
atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60  
tctcacatgc ggtggcatat ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120  
aaatggaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180  
gaataaagat aaaaaagaga aggacattac aaagggtggtc ctgacctttg ataaatctca 240  
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300  
ttgtggagct tctccctgag agagagtcct tgatctccca aaatttggtt gagatgtaag 360  
gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403  
<211> 303  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(303)  
<223> n = A,T,C or G

<400> 403  
cagtatttat agcnaactg aaaagctagt agcaggcaag tctcaaattc aggcacccaa 60  
tcctaagcaa gagccatggc atgggtgaaa tgcaaaaggga gagtctggcc aatctacaaa 120  
tagagaacaa gacctactca gtcatagaaca aaaaggcaga caccaacatg gatctcatgg 180  
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240  
tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300  
gga 303

<210> 404  
<211> 225  
<212> DNA  
<213> Homo sapiens

<400> 404  
aagtgttaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60  
attgttaatg cactcattta cctttacatg gtgaaagtgc tctcttgatc ctacaaacag 120  
acattttcca ctcgtgtttc catagtgtgt aagtgtatca gatgtgttgg gcatgtgaat 180  
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405  
<211> 334  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1) ... (334)  
<223> n = A,T,C or G

<400> 405  
gagctgttat actgtgagtt ctactaggaa atcatcaaatt ctgagggttg tctggaggac 60  
ttcaatacac ctcccccat agtgaatcag cttccagggg gtccagtcct tctccttact 120  
tcatccccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggg 180  
ttcccagtgct ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtg 240  
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagcccatgt 300  
cactctccac tctctcannn tggatccccac ccct 334

<210> 406  
<211> 216  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1) ... (216)  
<223> n = A,T,C or G

<400> 406  
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60  
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120  
acnaaacaca aattttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180  
actgccaaag aatnttcaag aaggaggact gccant 216

<210> 407  
<211> 413  
<212> DNA  
<213> Homo sapiens

<400> 407  
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60  
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120  
gtacaacatt gcacccagtg tcagattcta cacctggcca ctgaggaagc aagagttaat 180  
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240

ggaaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300  
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt ttctctgtca 360  
tgggagttcc agaaaaagt aaacagaca atgggcccagg ttctgtagta aag 413

<210> 408

<211> 183

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(183)

<223> n = A,T,C or G

<400> 408

ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60  
tncttaacta gttaatcctt aaagggtan ntaatcctta actagtcctt ccattgtgag 120  
cattatcctt ccagtattcn ccttctnttt tatttactcc ttctgggcta cccatgtact 180  
ntt 183

<210> 409

<211> 250

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(250)

<223> n = A,T,C or G

<400> 409

cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60  
gtgggttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120  
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180  
gcttccagtg gccccagga cagcgtgggc tatgtttaca ggccttcctt gctggggggg 240  
ggcctatgc 250

<210> 410

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(306)

<223> n = A,T,C or G

<400> 410

ggctgggttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60  
agtcttgcaa tccatttgc aggatccgtc tgtgcacatg cctctgtaga gaggcagcatt 120  
cccagggaacc ttggaaacag ttggcactgt aagggtgctt ctccccaaga cacatcctaa 180  
aagggtgttg aatgggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240  
nactgggttg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300  
tcntgc 306

<210> 411  
<211> 261  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(261)  
<223> n = A,T,C or G

<400> 411  
agagatattt cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60  
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120  
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180  
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240  
cttctctcaa ggngaggcaa a 261

<210> 412  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(241)  
<223> n = A,T,C or G

<400> 412  
gttcaatggt acctgacatt tctacaacac ccactcacc gatgtattcg ttgccagtg 60  
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgccagg aaatactacg 120  
actgaatttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180  
ctgggagatt tctctgggta cattgaattc ccaaactacc cangcaatta cccagccaac 240  
a 241

<210> 413  
<211> 231  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(231)  
<223> n = A,T,C or G

<400> 413  
aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60  
ctcatccaag tttctagtag cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120  
aagtttactc tctctatttg gaacctaaaa actctcttct tcttgggtct gagggctcca 180  
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414  
<211> 234  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 414

```
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttcctttgg catgggatgg ggatgaagta aggagaggga 180
ctggaccccc tggaagctga ttcactatgg ggggagggtg attgaagtcc tcca      234
```

&lt;210&gt; 415

&lt;211&gt; 217

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(217)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 415

```
gcataggatt aagactgagt atcttttcta cattctttta acttttctaag gggcacttct 60
caaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cacttttctca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggg tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc      217
```

&lt;210&gt; 416

&lt;211&gt; 213

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(213)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 416

```
atgcatatnt aaagganact gcctcgcttt tagaagacat ctggngctgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag      213
```

&lt;210&gt; 417

&lt;211&gt; 303

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(303)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 417

```
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
gtgggaaagg ctttactctg agttcaaatc ttcaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300
agt      303
```



<210> 418  
<211> 328  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(328)  
<223> n = A,T,C or G

<400> 418  
tttttggcgg tgggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60  
tgcacaggca tgatctcggc tcactacaac ccctgcctcc catgtccaag cgattcttgt 120  
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacacca gctagttttt 180  
gtatttttag tagagacagg gtttcaccat gttggccagg ctgggtctcaa actcctnacc 240  
tcagnggtca ggctggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300  
aaagtgctan gattacaggc cgtgagcc 328

<210> 419  
<211> 389  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(389)  
<223> n = A,T,C or G

<400> 419  
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatag 60  
acccttgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120  
cttgtttcct ctctgtggct ccattcatag cacagtgtgt gcaactgaggc ttgtgcaggc 180  
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggt gtgccaggca 240  
ccggttctcc agccaccaac ctactcgtc cccgcaaatg gcacatcagt tcttctaccc 300  
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360  
tggcagccac tcnggctgtg tcgacgcgg 389

<210> 420  
<211> 408  
<212> DNA  
<213> Homo sapiens

<400> 420  
gttcctccta actcctgcc aacacagctc tctcaacat gagagctgca cccctcctcc 60  
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120  
gaagtgtact agccaaggag ttgaagtgtg tgactttggt gtttcggcat ggagaccgaa 180  
gtcccattga cacctttccc actgaccca taaaggaatc ctcatggcca caaggatttg 240  
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300  
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360  
acgttgaccg gactttgatg aagtgtctatg acaaacctgg caagcccg 408

<210> 421  
<211> 352  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 421

```
gctcaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggtct tttttgggtc cttcttctcc accacnatat acttgcatgc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacaggtg tagaaacaag 240
ggtgcaacat gaaatttctg ttcgtagca agtgcattgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttctt gg 352
```

<210> 422

<211> 337

<212> DNA

<213> Homo sapiens

<400> 422

```
atgccaccat gctggcaatg cagcgggagg tccaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcatagacaa ggtgccggcg atcgcgggcg cgtcaatcct ggccaaggct agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggtc 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaatttat 337
```

<210> 423

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(310)

<223> n = A,T,C or G

<400> 423

```
gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggcctggcct gggagccctg tgccctactan aagcncatta gattatccat 120
tcactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
tccgagttta 310
```

<210> 424

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(370)

<223> n = A,T,C or G

&lt;400&gt; 424

```
ggtcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180
ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
cacgaaggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgacg                                     370
```

&lt;210&gt; 425

&lt;211&gt; 216

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(216)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 425

```
aattgctatn ntatttttg ccaactcaaaa taattaccaa aaaaaaaaaa tnttaaataga 60
taacaacnca acatcaaggn aaananaaca ggaatggntg acntngcata aatnggccga 120
anattatcca ttatnttaag gggtgacttc aggntacagc acacagacaa acatgcccag 180
gaggntntca ggaccgctcg atgtnttntg aggagg                                     216
```

&lt;210&gt; 426

&lt;211&gt; 596

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 426

```
cttccagtga ggataaccct gttgccccgg gccgagggtc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gcccgaaggg tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatgggta 180
gctgtccttg tattttgatt aacctaattg ccttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggcca ttaagaggca cttcccgtta 300
ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
gggtgatggc cttttcagct ttaacccaat ttgcaactgc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattgggt tactgcctga 540
gtcccgtcgg tcccaccca ggaccttcca tcggcgagta cctgggagcc cgtgct      596
```

&lt;210&gt; 427

&lt;211&gt; 107

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(107)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 427

```
gaagaattca agtttaggttt attcaaaggg cttacngaga atcctanacc caggncccag 60
```

cccgggagca gccttanaga gctcctgttt gactgcccgg ctcagng

107

&lt;210&gt; 428

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(38)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 428

gaacttcna anaangactt tattcactat tttacatt

38

&lt;210&gt; 429

&lt;211&gt; 544

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 429

ctttgctgga cgggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60  
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120  
atatccacga actcctgaag gactttctga tttatccaca atcaaatacat cggttttcag 180  
tttggtcgtt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240  
gccttccact tcagttacac ctcaactcacc atcctctcct gttgggtctg tgctgcttca 300  
agataactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360  
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagccac 420  
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480  
acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccagggtg gtaggagaga 544  
ttat

&lt;210&gt; 430

&lt;211&gt; 507

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(507)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 430

cttatcncaa tggggctccc aaacttggtt gtgcagtgga aactccgggg gaattttgaa 60  
gaacactgac acccatcttc caccgccaca ctctgattta attgggctgc agtgagaaca 120  
gagcatcaat ttaaaaagct gccagaatg ttntcctggg cagcgttgtg atctttgccn 180  
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240  
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300  
caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360  
tgtcagtga tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420  
cattctcctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480  
ttttgagcaa aaaaaaaaaa aaaaaaa 507

&lt;210&gt; 431

&lt;211&gt; 392

<212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(392)  
 <223> n = A,T,C or G

<400> 431  
 gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60  
 aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120  
 tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180  
 aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240  
 catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300  
 acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360  
 gcaatgagtc tggcttttac tctgctgttt ct 392

<210> 432  
 <211> 387  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(387)  
 <223> n = A,T,C or G

<400> 432  
 ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60  
 aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120  
 ngtagtccaa gctctcggna gtccagccac tngaaacat gctcccttta gattaacctc 180  
 gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240  
 attctgttgc ttctggggca ttctcttng atgcagagga ccaccacaca gatgacagca 300  
 atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgta aggaccggga 360  
 acaacgtata gaacactgga gtccttt 387

<210> 433  
 <211> 281  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(281)  
 <223> n = A,T,C or G

<400> 433  
 ttcaactagc anagaanact gcttcagggg gtgtaaaatg aaaggcttcc acgcagttat 60  
 ctgattaaag aacactaaga gaggggacaag gctagaagcc gcaggatgtc tacactatag 120  
 caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180  
 atcgccgtgg ctattcctcn ttgntattac accagngagg ntctctgtnt gccactgggt 240  
 tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

<210> 434  
 <211> 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 434

```
ttttaaaata agcatttagt gctcagtcctt tactgagtag tctttctctc ccctcctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120
tggtgcacaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtaga tccatcttgc 180
tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acagggtgaat tggatgggtc tcagaacccat ttcacccaga 300
cagcctgttt ctatcctgtt taataaatta gtttggtgtc tctacatgca taacaaaccc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag tacccatgtc 480
ttaa
```

484

&lt;210&gt; 435

&lt;211&gt; 424

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 435

```
gcgcccgtca gagcaggtea ctttctgcct tccacgtcct ctttcaagga agccccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccacacaa 120
cgatcgggca agtaaacccc ctccctcgcc gacttcggaa ctggcgagag ttcagcgcag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcattggtc ggggtgaccc 240
cttggagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaaacctt ggactcccca tgctctaact cccacactct 360
gctatcagaa acttaaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac
```

424

&lt;210&gt; 436

&lt;211&gt; 667

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(667)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 436

```
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcttc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccaggtttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
tgttcatgtt tataggactc attcaagaat tttctatatc tctttcttat atactctcca 420
agttcataat gctgctccat gccagctggg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggtcagt gggaaagggt tcaatgggac ttcgggtctc atgccgaaac 540
accaaagtca caaacttcaa ctcttggt agtacacttc ggtctagcca gaaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
tgtag
```

667

&lt;210&gt; 437

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 437

```
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc acactaggac tctaccatac cgggttttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtactcct ctattttcac ccctcttgct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatggt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttggggggac agccagcatc tttagctttc 420
atttgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540
tcctattttc aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc                                     693
```

&lt;210&gt; 438

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 438

```
ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac ctctcgtgact 60
ttatgcaatg catcatgcta ttccatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaaag acaactgcc aagaatcttc aagaaggagg 180
actgcaagta tatctgggtg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360
```

&lt;210&gt; 439

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(431)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 439

```
gttcctnnta actcctgcc a gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtc tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccatgta cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t                                     431
```

&lt;210&gt; 440

&lt;211&gt; 523

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 440

```

agagataaag cttagggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaattgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttacccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcctggaaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaat acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta 523

```

&lt;210&gt; 441

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 441

```

gttcctccta actcctgcc aaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtgtg tgactttggg gtttcggcat ggagaccgaa 180
gtcccatatga cacctttccc actgacccca taaaggaaac ctcattggca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gaggcttata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgctga cgcggccgcg 420
aathtagtag 430

```

&lt;210&gt; 442

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 442

```

ctaaggaatt agtagtgctc ccatcacttg tttggagtgt gctatttctaa aagattttga 60
tttcttgcaa tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attagctat 180
atgttttagaa atgggtcattt tacggaaaaa ttgaaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aattttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362

```

&lt;210&gt; 443

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(624)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 443

```

tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaa taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240

```



```
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaataaac 360
taacgcctac aaaacactta aacatagata acatagggtgc aagtactatg tatctggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga ggggaagggtt cctggaaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatac                                     624
```

<210> 444  
<211> 425  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(425)  
<223> n = A,T,C or G

```
<400> 444
gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtggtg gtcagcaaat ccttgaatgc 180
tgcttaatgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacacctg gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggtcgcag cggccgcgaa tttagtagta 420
gtaga                                     425
```

<210> 445  
<211> 414  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(414)  
<223> n = A,T,C or G

```
<400> 445
catgtttatg nttttggatt actttgggca cctagtgttt ctaaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcattgtggc agattattgg atgtagtctt ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtgggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaataact aggtctctcc tcttgtattt tgaagcagtg 360
tgggtgctgg attgataaaa aaaaaaaaaa tgcagcgcgc cgcaattta gtag 414
```

<210> 446  
<211> 631  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(631)

<223> n = A,T,C or G

<400> 446

```
acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcagggtgtg 120
atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgtttgttc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
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gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatgtt tcacagtggc tggactaccg agagcttggg ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccctg cattttgtgg 540
aatctacacc aatgaaaaca tgtactacag ctatatattg tttatgtatg atatatttga 600
aatagtatac attgtcttga tgttttttct g                                     631
```

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 447

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cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taaggggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggacgggat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccagggttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggcta gtacacttcg gtcta                                     585
```

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 448

```
tgctcgtggg tcattctgan nnccgaactg accntgccag ccctgccgan gggccnccat 60
ggctccctag tgccttgagg agganggggc tag                                     93
```

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(706)  
 <223> n = A,T,C or G

<400> 449  
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 ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120  
 cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180  
 cggggacagc atcctgcaga tggtcgggag cgcccattc gccattcagg ctgcgcaact 240  
 gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300  
 gtgctgcaag gcgattaagt tgggtaacgc caggggtttc ccagtcncga cgttgtaaaa 360  
 cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcattgcacg 420  
 cgtacgtaag cttggatcct ctagagcggc cgccactac tactaaattc gcggccgcgt 480  
 cgacgtggga tccnactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540  
 cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600  
 aacaggttga accctggagg tggagggtgc aatgagctga gatcaggccn ctgcncacca 660  
 gcatggatga cagagtgaag ctccatctta aaaaaaaaaa aaaaaa 706

<210> 450  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 450  
 gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60  
 acagttttta aaggtaaaac aacataaaaa gaaatatcct atagtggaaa taagagagtc 120  
 aaatgaggct gagaacttta caaaggagat ttacagacat gtcgccaata tcaactgcatg 180  
 agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240  
 caagtcagggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300  
 agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360  
 tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420  
 tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggg cgacgcggcc 480  
 gcgaatttag tag 493

<210> 451  
 <211> 501  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 451  
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 ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120  
 aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180  
 tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240  
 gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300  
 tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360  
 cgcncagac actcacagct actcaggagg ctgagaacag gttgaacctg ggagggtggag 420  
 gttgcaatga gctgagatca ggccnctgcn ccccgagcat gatgacagag tgaaactcca 480

tcttaaaaaa aaaaaaaaaa a

501

<210> 452

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(51)

<223> n = A,T,C or G

<400> 452

agacggtttc accnttaca cnccttttag gatgggnntt ggggagcaag c

51

<210> 453

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(317)

<223> n = A,T,C or G

<400> 453

tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60  
acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaaccat 120  
ttcaccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180  
taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240  
cccacaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300  
taccatgtc tttatta 317

<210> 454

<211> 231

<212> DNA

<213> Homo sapiens

<400> 454

ttcgaggtac aatcaactct cagagtgtag tttccttcta tagatgagtc agcatthaata 60  
taagccacgc cagctcttg aaggagtctt gaattctcct ctgtcactc agtagaacca 120  
agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180  
ccttcctttt tcagtgttcc aaagctcctc acaatttcat gaacaacagc t 231

<210> 455

<211> 231

<212> DNA

<213> Homo sapiens

<400> 455

taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60  
cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120  
gtttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180  
caaagaattt ctcatagcac agctcacaat acagggtcctc tttctcctct a 231

<210> 456  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 456  
ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60  
ttccattcag tattatcggt attattcttg gagaaaccct gtctgtttac tgtaaccttt 120  
tgcactcaaa ttcctttatc aggaataact acatagccac tatttacaaa gccattggaa 180  
cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaag t 231

<210> 457  
<211> 231  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(231)  
<223> n = A,T,C or G

<400> 457  
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gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catcacgttt 120  
tatttgattt tatttagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180  
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgc g 231

<210> 458  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 458  
aggtctggtt cccccactt ccactccctt ctactctctc taggactggg ctgggccaag 60  
agaagagggg tggtaggga agccgttgag acctgaagcc ccaccctcta ccttccttca 120  
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180  
ggtcctgggt taggcatttt ggggggccag accccaggag aagaagattc t 231

<210> 459  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 459  
ggtaccgagg ctgctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60  
ccttcgcaaa acctgtggtg gccaccagt cctaacggga caggacagag agacagagca 120  
gccttgcaat gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180  
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 460

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gcagggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaa 120
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231
```

&lt;210&gt; 461

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 461

```
cgagggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggaggggc 60
gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg 120
gtgggggttca gtgaggagtg ggaaattggg tcagcagaac caagccgttg ggtgaataag 180
aggggggattc catggcactg atagagccct atagtttcag agctgggaat t 231
```

&lt;210&gt; 462

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 462

```
aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
gggtcatgca agtataaaaa ttaaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120
gaagaactgt tagagagacc aacagggtag tgggttagag atttcagag tcttacattt 180
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231
```

&lt;210&gt; 463

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 463

```
tactccagcc tggtgacaga gcgagaccct atcacgccc cccacccac caaaaaaaaa 60
actgagtaga cagggtgtcct ctggcatgg taagtcttaa gtccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cgggtgtccc atctgagtga gaaaaggcag 180
tggggagggtg gatcttccag tcgaagcggg atagaagccc gtgtgaaaag c 231
```

&lt;210&gt; 464

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 464

```
gtactctaag attttatcta agttgccttt tctgggtggg aaagtttaac cttagtgact 60
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 120
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
gggtgccagcg caccagctag atgctctgta acttctaggc cccattttcc c 231
```

&lt;210&gt; 465

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 465

```

catgttggtg tagctgtggt aatgctggct gcatctcaga caggggtaac ttcagctcct 60
gtggcaaat agcaacaaat tctgacatca tatttatggt ttctgtatct ttgttgatga 120
aggatggcac aatttttgct tgtgttcata atatactcag attagttcag ctccatcaga 180
taaactggag acatgcagga cattagggta gtgtgttagc tctggtaatg a 231

```

&lt;210&gt; 466

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 466

```

caggtacctc tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60
ggccttcgaa cagaacttgc cacataccca ggtataatag tttctaacat ttgcccagga 120
cctgtgcaat caaatattgt ggagaattcc cttagctggag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcgtt gtgtgcggct g 231

```

&lt;210&gt; 467

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 467

```

gtacaccctg gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg 60
tggcggcttt tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac 120
tgtgccttaa cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180
gcatgggtct ctgcccgaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240
tgtgacctgc tgggcctccc aatagactaa caggcagtg cagtggacc caagagaaga 300
ctgcagcaga c 311

```

&lt;210&gt; 468

&lt;211&gt; 3112

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 468

```

cattgtgttg ggagaaaaac agagggggaga tttgtgtggc tgcagccgag ggagaccagg 60
aagatctgca tgggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120
tggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180
atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtgggtcaa 240
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gtgaatgtgg atgattggat gatcatttct catctctgag cctcaggttc cccatccata 360
aaatgggata cacagtatga tctataaagt gggatatagt atgatctact tcaactgggtt 420
atttgaagga tgaattgaga taatttattt caggtgccta gaacaatgcc cagattagta 480
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tccaaagcca acgtcgaatt ttgaaacata tcaaagctct tcttcaagac aaataatcta 1140
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```

```

tttagctctc aaaatgggtc attttaagag aaagtttttag aatctcatat ttattcctgt 1260
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tttgtccctg tagttaattg aaagaaatag ggcactcttg tgagccactt tagggttcac 3060
tcctggcaat aaagaattta caaagagcaa aaaaaaaaaa aaaaaaaaaa aa 3112

```

&lt;210&gt; 469

&lt;211&gt; 2229

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 469

```

agctctttgt aaattcttta ttgccaggag tgaaccctaa agtggctcac aagagtgcc 60
tatttctttc aattaactac aaggacaaac acatctcaaa gttgagataa gtgaccagta 120
tgatttgcca aaattctaaa gcgcactcac catgaaatgg ataaaggcta cttttgggga 180
tttgactgct atgaattctg tgaaaagctt gttggatatt gtgatagaga tagagaaatg 240
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```

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&lt;210&gt; 470

&lt;211&gt; 2426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 470

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2426

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&lt;210&gt; 471

&lt;211&gt; 812

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 471

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caciaaatct ccctctggtt ttctgatgcc ag
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&lt;210&gt; 472

&lt;211&gt; 515

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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(515)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 472

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gaaaaaaaaa naaaaaaaaa aaanaaaaan aaaaaa 515

**PCT**WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau

## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>7</sup> :</b> <b>C12N 15/12, C07K 14/47, C12Q 1/68, A61K 39/395, G01N 33/68, 33/574, C07K 16/30, C12N 15/62, 5/02 // A61P 35/00</b>		<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 00/04149</b> <b>(43) International Publication Date:</b> 27 January 2000 (27.01.00)																					
<b>(21) International Application Number:</b> PCT/US99/15838 <b>(22) International Filing Date:</b> 14 July 1999 (14.07.99)		<b>(74) Agents:</b> MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).																						
<b>(30) Priority Data:</b> <table border="0"><tr><td>09/115,453</td><td>14 July 1998 (14.07.98)</td><td>US</td></tr><tr><td>09/116,134</td><td>14 July 1998 (14.07.98)</td><td>US</td></tr><tr><td>09/159,822</td><td>23 September 1998 (23.09.98)</td><td>US</td></tr><tr><td>09/159,812</td><td>23 September 1998 (23.09.98)</td><td>US</td></tr><tr><td>09/232,880</td><td>15 January 1999 (15.01.99)</td><td>US</td></tr><tr><td>09/232,149</td><td>15 January 1999 (15.01.99)</td><td>US</td></tr><tr><td>09/288,946</td><td>9 April 1999 (09.04.99)</td><td>US</td></tr></table>		09/115,453	14 July 1998 (14.07.98)	US	09/116,134	14 July 1998 (14.07.98)	US	09/159,822	23 September 1998 (23.09.98)	US	09/159,812	23 September 1998 (23.09.98)	US	09/232,880	15 January 1999 (15.01.99)	US	09/232,149	15 January 1999 (15.01.99)	US	09/288,946	9 April 1999 (09.04.99)	US	<b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
09/115,453	14 July 1998 (14.07.98)	US																						
09/116,134	14 July 1998 (14.07.98)	US																						
09/159,822	23 September 1998 (23.09.98)	US																						
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09/232,149	15 January 1999 (15.01.99)	US																						
09/288,946	9 April 1999 (09.04.99)	US																						
<b>(71) Applicant:</b> CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).		<b>Published</b> <i>With international search report.</i>																						
<b>(72) Inventors:</b> DILLON, Davin, Clifford; 21607 N.E. 24th Street, Redmond, WA 98053 (US). HARLOCKER, Susan, Louise; 6203 20th Avenue N.W., Seattle, WA 98107 (US). YUQIU, Jiang; 5001 South 232nd Street, Kent, WA 98032 (US). XU, Jiangchun; 15805 S.E. 43rd Place, Bellevue, WA 98006 (US). MITCHAM, Jennifer, Lynn; 16677 Northeast 88th Street, Redmond, WA 98052 (US).		<b>(88) Date of publication of the international search report:</b> 20 July 2000 (20.07.00)																						
<b>(54) Title:</b> COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER																								
<b>(57) Abstract</b> <p>Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.</p>																								

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EE	Estonia						

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/15838

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/47 C12Q1/68 A61K39/395 G01N33/68  
 G01N33/574 C07K16/30 C12N15/62 C12N5/02  
 //A61P35/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97 33909 A (CORIXA CORP) 18 September 1997 (1997-09-18)  the whole document ---	1-22, 29-31, 35-49, 53-79
A	SJOGREN H O: "Therapeutic immunization against cancer antigens using genetically engineered cells" IMMUNOTECHNOLOGY, vol. 3, no. 3, 1 October 1997 (1997-10-01), pages 161-172, XP004097000 ISSN: 1380-2933 the whole document --- -/-	23-28, 32-34, 53-57



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

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- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

\*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

\*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

\*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

\*&\* document member of the same patent family

Date of the actual completion of the international search

31 January 2000

Date of mailing of the international search report

04.05.00

Name and mailing address of the ISA

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Authorized officer

ANDRES S.M.

## INTERNATIONAL SEARCH REPORT

International Application No

PCT, JS 99/15838

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>CHU R S ET AL: "CPG OLIGODEOXYNUCLEOTIDES ACT AS ADJUVANTS THAT SWITCH ON T HELPER 1 (TH1) IMMUNITY" JOURNAL OF EXPERIMENTAL MEDICINE, vol. 186, no. 10, 1 November 1997 (1997-11-01), pages 1623-1631, XP002910130 ISSN: 0022-1007 the whole document</p> <p>---</p>	14-20, 25-27, 41-47
A	<p>EP 0 317 141 A (BECTON DICKINSON CO) 24 May 1989 (1989-05-24) the whole document</p> <p>---</p>	50-52
A	<p>ZITVOGEL L ET AL: "Eradication of established murine tumors using a novel cell-free vaccine: dendritic cell-derived exosomes" NATURE MEDICINE, vol. 4, no. 5, 1 May 1998 (1998-05-01), pages 594-600, XP002085387 ISSN: 1078-8956 cited in the application</p> <p>---</p>	
P,X	<p>WO 98 37093 A (CORIXA CORP) 27 August 1998 (1998-08-27)</p> <p>---</p> <p>page 3, line 20 -page 22, line 2 page 35, line 9 - last line page 76, line 34 -page 78, line 22 claims</p> <p>---</p>	1-15, 17-19, 21,22, 29-31, 34,35, 39-42, 44-46, 48,49, 58-79
P,X	<p>WO 98 37418 A (CORIXA CORP) 27 August 1998 (1998-08-27)</p> <p>---</p> <p>page 2 -page 24 example 2 page 35, line 15 -page 36, line 11 page 81, line 14 -page 83, line 11 claims</p> <p>-----</p>	1-15, 17-19, 21,22, 29-31, 34,35, 39-42, 44-46, 48,49, 58-79

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 99/ 15838

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
Remark: Although claims 29-34, 48-49, 52, 55-57  
are directed to a method of treatment of the human/animal  
body, the search has been carried out and based on the alleged  
effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such  
an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all  
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment  
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report  
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is  
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-79 all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.



## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

.....  
Invention 1. Claims: 1-79 (all partially)

A polypeptide comprising at least an immunogenic portion of a prostate tumor protein defined as SEQ ID 108 and which is encoded by the related SEQ IDs 2,3,107 (according to the Description of the Sequence Identifiers), fragments and variants thereof, fusion proteins comprising it, polynucleotides or oligonucleotides derived therefrom, antibodies or fragments thereof binding to the polypeptide, pharmaceutical compositions or vaccines comprising these products and their use in methods for inhibiting, monitoring or diagnosing the development of a prostate cancer, for removing tumor cells from a sample or for expanding and/or stimulating T-cells.

Inventions 2. to 439. Claims: 1-79 (all partially and as far as applicable)

As for subject 1. but concerning respectively SEQ IDs 1,4-106,109-111,115-171,173-175,177,179-305,307-315,326,328, 330,332-335,340-375,381,382 and 384-472.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/JS 99/15838

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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